STRENGTHENING AWARDS

Strengthening Awards are intended to enhance the ability of faculty of small and mid-sized institutions or of institutions in USDA-EPSCoR States who have not previously been successful in obtaining competitive grants from the NRICGP in receiving support for strengthening their research programs. The research must be in an area supported by the NRICGP. The following types of Strengthening Awards are available: Research Career Enhancement Awards (to fund sabbatical leaves); Equipment Grants (to supply 50% of the funds necessary to purchase one major piece of equipment within the cost range of $10,000-$100,000); Seed Grants (to collect preliminary data); and Strengthening Standard Research Project Grants (to support standard research projects). Applications for the Research Career Enhancement Awards, Equipment Grants and Seed Grants were reviewed together by multidisciplinary peer panels. Strengthening Standard Research Project applications were reviewed in the program area most appropriate for the type of research proposed; therefore, these nontechnical abstracts also appear under the respective program areas.

9703540 60Co Radiation Source for Food Safety Research
Weete, J.D.; Conner, D.; Weese, J.G. **Grant 97-35207-4618**

Auburn University **Equipment Grant**
Leach Science Center **$35,000**
Auburn, AL 36849-5318 **1 Year**

Gamma radiation can be an effective means of eliminating spoilage and disease-causing microorganisms from foods. Acquisition of 15,000 curies of cobalt-60 as a radioactive source will enable researchers to conduct research in which food products such as meat, poultry, and produce will be treated with radiation doses currently used in commercial applications (0.5-7kGY). The overall goal is to develop strategies for eliminating pathogens from food that are applicable to the commercial processing and also maintain (or improve) the sensory and nutritional quality of the food product. Specifically, this involves interdisciplinary research involving microbiologists, nutritionists, and food scientists. The interaction of common food handling/processing procedures and irradiation treatment on the safety, shelf-life, nutritional content, and sensory attributes of meat products and produce will be a main thrust of this research effort.

9703544 ICP-Atomic Emission Spectrometer for Nutrition Research
Barnes, D.M.; Kegley, E.B.; Oliver, K.G. **Grant 97-35207-4617**

University of Arkansas, Fayetteville **Equipment Grant**
Department of Poultry Science **$48,387**
Fayetteville, AR 72701 **1 Year**

The objective of this proposal is the acquisition of an Inductively Coupled Plasma Atomic Emission Spectrometer (ICP-AES) for the analysis of minerals in animal feeds, animal products and environmental samples. Our current facilities support many aspects of nutritional and environmental research, however, a rapid method for the analysis of trace elements is not currently available. In addition, sensitivity in the analysis of trace elements is becoming an important issue as research shows an increasing role in metabolism at very low concentrations. This instrument will increase our ability to rapidly detect very small potentially crucial differences in trace elements directly affecting animal performance.

The acquisition of an ICP will benefit research projects in the Department of Poultry Science, Animal Science, and Human Environmental Science including: (1) two projects that examine the impact of trace element pollutants on metabolism; (2) the role of heavy metals and other trace elements in immune function; and (3) dietary levels and effects of boron. The ICPAES system will also provide an essential training resource for undergraduate and graduate students in modern analytical instrumentation, through involvement in research projects and formal nutrition and environmental chemistry course work.

9703551 The FAIR Act of 1996: Impacts on Land Leasing
Dixon, B.L.; Ahrendsen, B.L.; Bierlen, R.W. **Grant 97-35402-4633**

University of Arkansas, Fayetteville **Seed Grant**
Department of Agricultural Economics and Agribusiness **$49,986**
Fayetteville, AR 72701 **2 Years**

Typically farmers have the option of either purchasing or leasing land. Leasing is important in all U.S. regions and currently about 43% of U.S. agricultural land is leased. On the individual farm, the quality of the leased land and the cost of leasing play a key role in determining profitability and competitiveness. The 1996 Farm Bill (FAIR ACT) dramatically changes financial support to farmers. There are also conflicting theories concerning how landlords and tenants decide among cash rent and share leases. A better understanding of the leasing process would be helpful to agricultural policy makers, landlords and tenants. Data will be collected from eastern Arkansas farmers and landlords concerning their lease agreements with the intention of clarifying important issues and testing hypotheses. Eastern Arkansas is crop-intensive, crop selection is diverse and individual crops are important on the national level, rental acres are significant for most farmers, and most operations are large which is the class of farms most dependent on leasing. Considerable attention in the questionnaire will be devoted to ascertaining the changes in leasing due to the FAIR Act. Additional information will be gathered to find support for theories which explain how landlords and tenants decide among cash rent and share arrangements. Data will be collected in collaboration with National Agricultural Statistics Service (NASS) in Arkansas which has significant survey experience. Other project tasks will be performed at the University of Arkansas-Fayetteville. Our long-run goal is to expand the study to a regional or national level using the Arkansas study as a base.

9703472 Selective Channeling of Chicken Immunity to Inflammatory Versus Antibody Making Pathways
Durdik, J.M. **Grant 97-35208-4701**

University of Arkansas, Fayetteville **Seed Grant**
Department of Biological Sciences **$50,000**
Fayetteville, AR 72701-3018 **2 Years**

The immune system has two major and separate pathways for fighting off infections. One pathway results in the immune system making large quantities of antibodies and the other in making inflammatory cells that directly fight off the infection. Whether the immune response is dominated by one pathway or the other is often key to surviving infections. Helper T cells which can be either Thl or Th2, determine which pathway is chosen. For the inflammatory pathway, the Thl dominates and for the antibody pathway, the Th2 dominates. Very little is known about how Thl versus Th2 choices are controlled in domestic fowl. We will test if chickens can be immunized to activate, preferentially, either an antibody-dominated Th2 response or an inflammatory cell-dominated Thl response. We will use strategies known to shift the response in mice from Th2 to Thl pathways by delivering the vaccine preferentially to cells called macrophages. For this, we will use immunization of chickens with a live bacterium that rapidly enters macrophages. If we first kill the bacteria we expect a Th2-dominated response instead. We will also chemically modify our vaccines so that they bind to scavenger receptors present on macrophages in many animal species. We will use assays for inflammatory versus antibodymaking responses, as well as assays for the ability of T cells to activate macrophages, help B cells make antibodies, and express small hormone-like molecules. Together, these data will provide a system for investigating the control of Thl versus Th2 pathways in chickens, and will contribute significantly in the development of better vaccines for poultry diseases.

9703427 Acquisition of a Gas Chromatograph to Enhance Research in Forest and Range Ecosystems
Evans, R.D. **Grant 97-35106-5148**

University of Arkansas **Equipment Grant**
Biological Sciences **$22,507**
Fayetteville, AR 72701 **1 Year**

A gas chromatograph is essential to study the input, loss, and transformation of nitrogen and carbon in terrestrial ecosystems. A gas chromatograph is requested to study mechanisms controlling input of nitrogen from nitrogen fixation, loss of nitrogen from denitrification, and transformations of nitrogen by the soil microbial pool in range and forest ecosystems. This equipment will allow us to pursue research questions and future funding in areas that are directly applicable to the goals of the NRICGP. Research in rangelands of the western United States focuses on the long-term consequences of grazing and the impact of plant invasion on nitrogen cycling and plant nitrogen availability. The requested equipment will facilitate experiments that quantify changes in nitrogen input from nitrogen fixation, and the factors that control activity of the soil microbial pool. This work will allow us to evaluate the integrity and function of rangelands. Research in the Ozark Highlands addresses the impact of NO_3^- pollution from poultry production on nitrogen cycling in economically-important forest ecosystems. The gas chromatograph will allow us to assess how nitrogen input from the poultry industry has altered soil transformations and nitrogen loss from neighboring forest ecosystems, and the capacity of these ecosystems to buffer excess nitrogen input. Experiments using the gas chromatograph will provide the mechanistic understanding of factors controlling the input, transformation, and loss of nitrogen in these range and forest ecosystems that is necessary to understand the long-term stability and sustainability of managed ecosystems and their potential response to anthropogenic change.

9703433 Addition of HPLC Equipment for Expanding Research Capabilities
Lavy, T.; Mattice, J.; Brigg, B. **Grant 97-35106-5146**

Arkansas Agricultural Experiment Station **Equipment Grant**
Department of Agronomy **$30,212**
Fayetteville, AR 72704 **1 Year**

Following are areas in our laboratory which will greatly benefit from the availability of the new equipment provided by this grant: 1) Properly disposing of pesticide wastes is an important issue from both environmental and legal standpoints. We have developed functional ozonation systems for removing pesticides from the original spray mixture, but it is essential that breakdown products be identified to assure that these end products are less toxic than the parent compound. 2)Although most rice pesticides degrade readily in the environment, information providing an in-depth evaluation of their breakdown products is lacking. 3) Our 319 EPA demonstration project will involve a Best Management Plans (BMP) to control soil erosion in cotton fields using no till and reduced till techniques. This updated HPLC diode array equipment will allow us to monitor for these new pesticides which are vital to the reduced-till concept. 4) Development of a new biological means for controlling rice weeds in a flooded setting will be assisted by HPLC photodiode array. In flooded fields, a sharp, weed free circle surrounding clusters of certain rice lines provides visual evidence of weed toxins associated with rice growth. Identifying these weed toxins and developing a rapid screen

for them will help researchers. Development of natural plant compounds toxic to weeds could decrease our reliance on synthetic weed control compounds.5) Several of our graduate students have the academic background, desire, and research need to utilize this new equipment in their research programs. Industry continues to seek our technically trained individuals who possess a variety of analytical instrumental experiences.

9703458 Total Vineyard Mechanization to Optimize Yield and Quality of Grape Production
Morris, J.R. **Grant 97-35501-4635**

University of Arkansas, Fayetteville **Equipment Grant**
Institute of Food Science and Engineering **$4,903**
Fayetteville, AR 72704-5585 **1 Year**

This equipment grant will help purchase components of an Oldridge Total Vineyard Mechanization System. This equipment will be used in current vineyard mechanization efforts on Concord grapes. In order for processors to maintain a consistent product from year to year, it is necessary to have a similar quality of grapes each year. The effects that total vineyard mechanization will have on vine, fruit, juice and wine quality have not been established. This equipment will be used in vineyard studies, and raw product and grape juice quality will be monitored to ensure that quality can be maintained. The widespread conversion of vineyards to totally mechanized systems, without study, could result in a decline in juice and wine quality. Arkansas is unique as a grape growing state because all grape species can be grown here. This means that mechanization research from Arkansas is applicable from the East Coast to the West Coast and beyond. The University of Arkansas is well known for its efforts in the area of vineyard mechanization and has been chosen by the American Enology and Viticulture Research Network (AVERN) to lead a national effort in vineyard mechanization.

9702311 Functional Analysis of MDV pp24/pp38-Encoding Genes
Parcells, M.S. **Grant 97-35204-5067**

University of Arkansas, Fayetteville **Strengthening Award**
Department of Poultry Science **$185,000**
Fayetteville, AR 72701-1201 **3 Years**

Marek's disease (MD) is a cancer of chickens caused by Marek's disease virus (MDV), a cell-associated herpes virus. MD is a major concern to the poultry industry because tumor-bearing chickens are condemned at processing. MDV-induced tumors are comprised of transformed T-lymphocytes. How MDV transforms these T-cells is currently unknown, but studies examining what MDV genes are active in the tumors and cell-lines established from these tumors have identified a number of potential oncogenes. Two such genes encode phosphorylated proteins pp24 and pp38. The genes encoding these proteins span the segments of repeated DNA sequence flanking a region of long unique sequence. Thus, the first 62 amino acids of pp24 and pp38 are identical but the rest of the proteins are quite different. To understand the function of these genes, we plan to interrupt each gene by inserting a marker gene into the unique regions of each protein. Finally, we plan to interrupt both genes by inserting our marker gene in front of the region that is common to both genes. The marker gene that we plan to use encodes a modified Green Fluorescent Protein, a naturally-fluorescent protein originally isolated from a jellyfish, *Aequorea victoria*. This marker gene will allow us to follow the mutant MDVs through their infection of chickens to identify what abilities may be lost when the pp24- or pp38-encoding genes are disrupted. Through our study of these viruses, we hope to learn the function of these genes as they relate to MDV infection, pathogenicity and tumor-formation.

9703786 Design of an Agroforestry System with Structured Tree Clusters
Zeide, B.; Francis, P.; Kluender, R. **Grant 97-35108-5126**

University of Arkansas **Strengthening Award**
School of Forestry **$97,663**
Monticello, AR 71656-3468 **2 Years**

One tenth of the trees that a forester plants provides at the end of rotation about three quarters of all discounted returns. It is proposed to plant these crop trees (loblolly pine, *Pinus taeda* L., 50 per acre) surrounded by nurse trees (shortleaf pine, *Pinus echinata L.*). The area between rows of tree clusters is utilized for forage and beef production. The coexistence of trees, forage, and livestock is natural and can be mutually beneficial for several biological and managerial reasons. The objectives of this project are to determine tree spacing and schedules for tending trees (pruning and thinning), forage, and animals that will optimize economic, social, and ecological benefits. We will test three types of structured rows, four within-row distances, three thinning intensities, and three levels of pruning for two agroforestry systems (improved agro-silvicultural system and an agro-silvo-pastoral system) in three replications on a 30-acre field in southwestern Arkansas.

9703702 Management and Intensive Culture of Hybrid Striped Bass Fingerlings
Lochmann, S.E. **Grant 97-35208-4938**

University of Arkansas, Pine Bluff **Seed Grant**
Aquaculture and Fisheries Department **$49,772**
Pine Bluff, AR 71601 **2 Years**

The U. S. Department of Agriculture has been considering the aquaculture potential of striped bass *Morone saxatilis* and its hybrids with white bass *M. chrysops*. Several factors, including availability of fingerlings, constrain the successful development of the hybrid striped bass industry. Successful production of fingerlings is dependent upon the ability of a producer to provide fry with adequate amounts and types of live prey when their yolk reserves have been depleted. Unfortunately, the level of a producer's success is generally not known until the end of a six week production cycle. We propose to examine the potential of using fry condition measures as tools for monitoring the progress of fingerlings during the production cycle. This would result in cost savings and improved production stability as ponds which show indications for poor fry survival are either managed to improve survival or drained and restocked. Increasing the period of time during which fingerlings could be produced would also stabilize the industry, but variable weather conditions increase risk in some seasons. Therefore, several investigators have cultured fry indoor using cultured zooplankton as a food source. The effort and expense required for this method is considerable and, hence, impractical from a commercial perspective. We propose to use natural zooplankton from culture ponds as a food source for intensive indoor culture of fingerlings. To our knowledge, the indoor production of sunshine bass fingerlings using zooplankton harvested from outdoor culture ponds has not been attempted.

9701405 Genetic Control of Surface Lipid Biosynthesis in Sorghum
Jenks, M.A. **Grant 97-35301-4964**

Arkansas State University, State University **Strengthening Award**
College of Agriculture **$100,000**
State University, AR 72467 **2 Years**

Sorghum growers, like those of similar crops, suffer significant losses to a variety of pathogenic fungi. Increasing fungicide use by US farmers is increasing the cost of crop production and leading to the accumulation of toxic residues in our soil and groundwater. Fungi are also developing resistance to currently used fungicides. Therefore, alternative methods are needed to protect crops from fungal pathogens. The diverse surface lipid coatings covering all aerial plant tissues likely play a key role in plant resistance to fungi. Genetic engineering should therefore be explored as a means of modifying crop surface lipids to improve crop pathogen-resistance. However, little is known about gene involvement in plant surface lipid biosynthesis, or the role these lipids play in plant pathogen-resistance.

This proposal plans to employ sorghum as a model crop system to elucidate gene involvement in the biosynthesis of surface lipids. Single and double mutants in sorghum will be analyzed using gas chromatography mass-spectrometry to describe substrate flow through, and gene product function in, surface lipid biosynthesis. Sorghum's predominance of free acids on the surface makes it an ideal model for dissecting wax precursor (acyl-CoA) elongation and associated reactions. In addition, these mutants will be employed in field and greenhouse studies to examine surface lipid involvement in sorghum susceptibility to three important crop fungi, *Exserohilum*, *Colletotrichum*, and *Gloeocercospora*. In the future, findings from this research will be used with genetic engineering to modify sorghum surface lipids and improve sorghum's pathogen resistance.

9703436 Characterization of the Tomato Water Stress Protein LE25
Bray, E.A. **Grant 97-35106-4765**

University of California, Riverside **Seed Grant**
Department of Botany and Plant Sciences **$50,000**
Riverside, CA 92521-0124 **2 Years**

Stresses in the environment, such as lack of water (water stress), limit plant growth and cause crop loss. Plants respond to a lack of water in many ways, and through these responses adapt to water stress. Examination of plant responses to water stress provides valuable information which may be exploited to produce crops in unfavorable environments. Production of specific proteins, which is one type of response, may permit survival and continued productivity of plants during stress. One protein, called LE25, is synthesized in leaves during water stress. Using biotechnology, unique properties of this protein may be exploited to improve stress tolerance of crop plants. The research that will be completed during the two-year-funding period will characterize the function of LE25 during water stress. An antibody will be made which is needed to determine the timing and amount of protein made during stress, and to facilitate purification of the protein. The structure of the purified protein will be determined. Previously developed yeast strains which accumulate LE25 have improved tolerance of salt and freezing stress. These strains will be further studied to determine if protein expression confers tolerance to additional environmental stresses. Finally, biotechnological techniques will be used to produce plants that accumulate increased quantities of LE25 to determine if this

protein has a function in adaptation to stress. The acquired knowledge will be applied to the development of crop plants that can be productive in unfavorable environments.

9702890 Continuous Application Technology - A New Approach for Biocontrol
Crowley, D.E. **Grant 97-35316-4944**

University of California, Riverside
Department of Soil and Environmental Sciences
Riverside, CA 92521

Strengthening Award
$160,000
2 Years

The use of plant disease suppressive microorganisms for biocontrol of plant pathogens is presently constrained by the poor survival and activity of microorganisms after their introduction into field soils. The proposed research will investigate novel technology which employs the continuous application of disease-suppressive bacteria to irrigated crops. This technology uses a field fermentation machine developed by EcoSoil Systems Inc. that automatically cultures large quantities of selected microorganisms on site (up to 109 cfu/ml), and then injects them automatically into the irrigation system. With this technology we can: 1) Apply *inoculum* at densities that will achieve biological control. 2) Apply organisms in a metabolic state that will achieve biological control. 3) Maintain high levels of biological control agent even where the agent might not survive. 4) Consistently deliver the biocontrol agents to the rooting area where they will be most effective. 5) eliminate the need for a long storage life of the biocontrol organism. Using this technology together
with our expertise on Phytophthora root rot of citrus, our objectives are: 1) to determine if the continuous application of the biocontrol agent Pseudomonas *putida* will enhance the control of Phytophthora root rot of citrus compared to single applications and no applications and 2) determine
the effect of continuous application of *P. putida* on soil characteristics and the indigenous microbial community. In order to accomplish these goals we will employ a combination of classical large scale field experimentation, greenhouse trials and novel molecular approaches.

9701695 Developing Guayule for Domestic Production of Value-Added, Hypoallergenic Latex
Estilai, A. **Grant 97-35504-5120**

University of California, Riverside
Department of Botany and Plant Sciences
Riverside, CA 92521-0124

Strengthening Award
$150,000
3 Years

Recently, a developing crisis has brought attention to guayule, a desert plant native to Mexico and Texas, as a possible source of hypoallergenic latex. Health and medical workers have developed allergic reactions to the proteins present in *Hevea* latex, a commercial source for manufacturing latex gloves and other latex products. Guayule latex has been reported to be free from those proteins. To commercialize guayule as a safe source of latex and solid rubber, the industry will need shrubs for latex extraction and development, a seed source for establishing large-scale guayule fields, and high-latex-yielding guayule lines that can compete with *Hevea.* The goals of this project are to develop guayule lines with increased latex production, to increase the seed output of the improved lines for large-scale planting, and to investigate the genetic basis of latex production in guayule. Plants will be screened for latex content using the genetically diverse University of California *Parthenium* collection, which consists of sexual diploid and apomictic polyploid guayule germplasms, and other related species. Crosses will be made between the high- and low-latex-producing genotypes, and the advanced and backcross generations will be used to determine the inheritance of latex production. High-latex-producing genotypes will be increased, and the seed will be used to establish large acreage of guayule. Success in this project could reduce our total dependence on foreign sources of natural rubber that costs the nation $1 billion annually. Also, having a renewable domestic source of latex that can be produced in the semiarid lands of the southwest can reduce our dependency on ever-diminishing petroleum oil to produce synthetic elastomers.

9701031 Selenium Biogeochemistry in a Semi-Arid Ecosystem: Mass Balances under Field Conditions
Frankenberger, W.T.; Jury, J.; Jury, W.A. **Grant 97-35107-4853**

University of California, Riverside
Department of Soil and Environmental Sciences
Riverside, CA 92521-0001

Strengthening Award
$230,000
2 Years

Selenium (Se) is a widespread contaminant throughout the western U.S. due to its occurrence in sediments and saline drainage water. It is toxic to mammals and birds at the high concentrations which are found in evaporation ponds, where Se is concentrated. Remediation of seleniferous soils and sediments is of extreme importance to the sustainability of U.S. agriculture for the next decade. Natural remediation might occur to a certain extent due to microbial activity, evolving methylated Se from soil (mainly dimethylselenide). However, biomethylation can be enhanced by (i) the amendment of specific organic C sources (e.g., pectin, zein, casein); and (ii) cultivation of specific vegetation stimulating microbial activity via root exudates and also volatilizing Se following uptake. A combination of these processes can be used as an effective bioremediation technology. Very little information

is available on the influence of vegetation and the rhizosphere on the biomethylation of Se. Generally, Se volatilization has been investigated in small laboratory systems under artificial and non-varying conditions. Field studies need to be conducted to reflect realistic conditions, including antagonistic processes (e.g., leaching, adsorption, and elemental precipitation).

Experiments will be conducted with a novel constructed wind tunnel, set up in the field above a lysimeter. A complete balance sheet under realistic outdoor conditions will be obtained. Se volatilization will be continuously monitored using activated charcoal traps. Simultaneously, Se movement in soil, its occurrence in leachate and uptake by vegetation as well as its biochemical conversion via microbial transformations will be investigated. The experimental plan includes the influence of different vegetation, soil amendments and climatic conditions on the biomethylation
of Se in the soil/plant system. All experimental data will be analyzed with a four compartment modeling approach (insoluble, soluble, volatilized and leached Se).

This project will address mass balances of Se subject to volatilization, leaching, adsorption, elemental precipitation and plant uptake. Information gained from this study will be useful in establishing *in situ* bioremediation technology for soils contaminated with Se.

9700852 Assessment and Emission Reduction of Methyl Bromide Alternative Fumigants
Gan, J.; Yates, S.R.; Becker, J.O.; Jury, W.A. **Grant 97-35107-4378**

University of California, Riverside **Strengthening Award**
Department of Soil and Environmental Sciences **$205,000**
Riverside, CA 92521-0001 **3 Years**

Soilborne plant pathogens and parasitic nematodes can cause extensive damage to many crops, especially in intensive agriculture. Over the last few decades, soil disinfestation has relied
on the use of chemical disinfectants, primarily fumigants. Due to their high vapor pressures, most of these compounds have inflicted negative effects on the environment or human beings. Recently, emissions of methyl bromide were implicated in stratospheric ozone depletion, and its use is scheduled for phase out in the US by 2001. Our lack of knowledge of the mechanisms underlying the environmental behavior of these volatile pesticides, and employment of application methods of high emission potentials, have clearly contributed to the many failures in the use of fumigants in modern agriculture. Since few non-chemical methods are available at this time, preserving the use of the few remaining fumigants by minimizing their negative environmental effects is of immediate importance.

The two most important alternatives to methyl bromide are 1,3-dichloropropene and methyl isothiocyanate, both classified as Clean Air Act substances, and both frequently detected in the air under current application practices. We propose to conduct laboratory, field and simulation studies to understand the variables that control fumigant transport and volatilization, and through manipulating these variables, develop feasible application-soil management protocols that will have adequate efficacy, but will allow significantly less emissions. Our research approach is multidisciplinary collaboration among soil physicists, chemists and plant scientists. The integration of environmental studies with evaluation of biological efficacy will assure applicability of the research results to real life scenarios.

9703941 DNA Sequencer in Pest Management
Gill, S.S.; Keen, N.T.; Cooksey, D.A. **Grant 97-35311-5150**

University of California, Riverside **Equipment Grant**
Department of Entomology **$42,243**
Riverside, CA 92521-03141 **1 Year**

This equipment grant will purchase an automated DNA sequencer to identify genes that may play crucial roles in pest management. This DNA sequencer will support three principal research areas, one in entomology and two in plant pathology. The first research area, the main focus of this grant, involves the identification of proteins that are expressed in the central nervous system of lepidopteran larvae. The focus of the laboratory would be the identification of proteins that have a significant role in insect pest management. Attempts will be made to identify the DNA sequences of known protein targets for existing insecticides. Identification of these DNA sequences may aid studies on insecticide resistance especially if such mechanisms are known to exist from physiological studies. Additionally these sequencing efforts will also attempt to identify other insect proteins that may be potential targets for new insecticides, and to identify proteins that play critical roles in insect development. The two plant pathology projects that will be supported by this DNA sequencer include characterization of bacterial genes involved in the biological control of plant pathogenic fungi and the elucidation of mechanism of bacterial pathogenicity on host plants.

9703543 Phosphorylated Prolactin in the Mammary Gland: An Autocrine Regulator?
Walker, A.M. **Grant 97-35208-4861**

University of California, Riverside **Seed Grant**
Biomedical Sciences **$50,000**
Riverside, CA 92521-0121 **2 years**

The aim of this research project is to establish the role of phosphorylated prolactin in the mammary gland. In two other, unrelated prolactin-responsive tissues, phosphorylated prolactin acts as an antagonist to non-phosphorylated prolactin. A determination of whether this is also true in the mammary gland, may permit the development of strategies to increase mammary growth and milk output. There are two ways in which mammary epithelial cells can be exposed to prolactin. The first of these is exposure of the basolateral surface to blood-borne prolactin, derived from the pituitary, most of which is non-phosphorylated. The second is exposure on the apical surface to milk prolactin, 85-100% of which has been reported to be phosphorylated. Interestingly, in non-pregnant, non-lactating women and in lactating animals, the majority of prolactin receptors have been demonstrated to be or appear to be on the apical surface, consistent with a potential response of the epithelial cells to milk/ductal fluid prolactin. Thus, mammary responsiveness may be a balance between basolateral and apical signaling, with this distinction becoming most acute once full polarization of these cells occurs. Since most of the milk prolactin is phosphorylated, signaling from milk would be predicted to be inhibitory to further milk production. Removal of this inhibitory influence due to suckling may contribute, along with the suckling induced rise in circulating prolactin (predominantly non-phosphorylated), to renewed milk production. This seed grant project will utilize polarized bovine mammary epithelial cells in culture to determine the functional consequences of apical or basolateral application of recombinant versions of non-phosphorylated and phosphorylated prolactin.

9702580 Vector Specificity and Semipersistent Closterovirus Transmission by Whiteflies
Walker, G.P.; Creamer, R. **Grant 97-35302-4966**

University of California, Riverside **Strengthening Award**
Department of Entomology **$100,000**
Riverside, CA 92521-0001 **3 Years**

Plant viruses transmitted by whiteflies are very vector-specific. For example, lettuce chlorosis virus (LCV) is transmitted only by two closely related whitefly species, silverleaf and sweetpotato whiteflies, but not by any other whitefly, and tomato infectious chlorosis virus (TICV) has only a single vector, greenhouse whitefly, and not any other whitefly species. The high degree of vector-specificity of whitefly-transmitted viruses indicates that transmission is dependent on very precise, specific mechanism(s) that enable a particular whitefly species to transmit a specific virus. This mechanism(s), therefore, is a critical link in the epidemiology of the virus, and if it can be disrupted, virus transmission can be prevented. In order to develop methodology to disrupt the mechanism(s), we must first know what the mechanism(s) is and how it functions. This study will determine the mechanism(s) by which viruses are transmitted by whiteflies, and how the mechanism(s) determines whether a whitefly species can or cannot transmit a virus. LCV and TICV and their specific whitefly vectors will be used as model systems. We will determine the specific behavioral event in the whitefly's complex feeding process that is responsible for virus transmission and determine if differences in this behavior result in a whitefly being a vector or nonvector. We will also determine the site of retention of the virus in the whitefly's body and determine if differential retention and subsequent release of the virus in the whitefly result in a whitefly being a vector or nonvector.

9703470 Development and Validation of an Ultrasensitive, Nonradiometric GnRH Assay
Beckett, J. L. **Grant 97-35208-5099**

California Polytechnic State University, San Luis Obispo **Equipment Grant**
Department of Animal Science **$18,500**
San Luis Obispo, CA 93407 **1 Year**

Reproduction begins as a cascade of endocrine events in the hypothalamus of the brain. Gonadotropin-releasing hormone (GnRH) is synthesized and secreted by the hypothalamus to act on the cells in the pituitary gland responsible for production and release of the gonadotropic hormones. Regulation of this reproductive cascade is possible at several sites along the pathway, including the release of GnRH from the hypothalamus. The levels of GnRH encountered are sufficiently low such that it is not currently possible to measure the levels of the hormone in the general circulation through minimally invasive methods. Recently, instruments have been developed which measure the release of light resulting from the reaction of chemiluminescent compounds. The detection of these chemiluminescent compounds by luminometers is extremely sensitive. By conjugating a luminescing agent to GnRH, a competitive assay may be developed in which antibodies specific for GnRH recognize the endogenous and conjugated GnRH. In the proposed assay, serum samples will be collected from animals and placed in microtiter plates coated with GnRH-antibodies. Following binding of the endogenous GnRH with the antibodies, GnRH conjugated with a chemiluminescent agent will be added. The endogenous and conjugated GnRH will compete for antibody binding sites. Unbound GnRH (both endogenous and conjugated) will be poured off, and a chemiluminescent activator will be added. The strength of light emission

will be detected compared with standard curves. After proper development and validation of this assay, the effects of environmental factors on GnRH secretion will be measurable thereby explaining suppressed reproductive function during nutritional, seasonal and prepubertal stressors.

9704006 The Purchase of a Beckman LF 3600 DT Protein Sequencing System
Chen, T.T. **Grant 97-35208-4918**

University of Connecticut **Equipment Grant**
Biotechnology Center **$33,800**
Storrs, CT 06269-3149

This grant to the Macromolecular Characterization Facility (MCF) of the University of Connecticut Biotechnology Center (UCBC) is to purchase a Beckman LF 3600DT Protein Sequencing System. This instrument is capable of removing one amino acid at a time from the molecular chain which comprises the parent protein and identifying it so that the sequential arrangement of the amino acids within the protein molecule can be determined. The chemistry used in the instrument to separate each amino acid from the protein chain was developed by Dr. Edman and is the most used method for removing an amino acid and altering it so that it can be identified unequivocally. The sequencer is comprised of three modules, the first, performs the reactions necessary to remove one amino acid from the protein chain commencing with the amino terminus, the second part, analyzes the removed amino acid and identifies it, and the third module, is the data storage system. The instrument is a state-of-the-art sequencer with a computer program written to direct and monitor the performance of the chemical section, the analysis section, and to collect, analyze, interpret and store the data. The software compares the sample data with the standard data provided for each of the 20 naturally occurring amino acids which make up natural proteins and then provides the sequence.

Samples of proteins or peptides from many different sources can be sequenced using this instrument. The samples may be available as solids, in buffer solution or they may be blotted onto special plastic membranes. The instrument is capable of analyzing protein samples in any of these forms and providing some length of sequence data. Within the body of the proposal, many of the sources for sample proteins and the uses to which sequence data on these may be put are more completely delineated.

The Beckman protein sequencer will be installed inside MCF and would be available to the scientific community, on or off campus, either as a protein sequencing service or for individual "hands-on" use. A fee would be charged for each sequencing cycle, the separation of an amino acid from the parent protein, its isolation and determination is considered a cycle. The price would recover the cost of consumables and the replacement of limited life components, such as, the HPLC column and/or the UV/V, its detector lamp as well as provide funds for repairs on the instrument and for the purchase of upgrades to the software or hardware. Dr. Franklin Mauri, Senior Facility Scientist, will operate the instrument, assist in sample preparation, in the evaluation of the purity of the protein preparation and in the performance of digestions of proteins whose amino terminus is altered so that the Edman chemistry will not attack the amino acid which occurs first on the protein molecule. He will also be available to train personnel in the use of the instrument and in the interpretation of the data obtained from a sequencing run.

9703049 Endothelin-1 and Bovine Luteolysis
Milvae, R.A. **Grant 97-35203-4856**

University of Connecticut **Strengthening Award**
Department of Animal Science, U-40 **$140,000**
Storrs, CT 06269-4040 **2 Years**

The long term goal of this research is to gain a better understanding of the processes controlling regression of the bovine corpus luteum (CL). Previous studies and results of our preliminary experiments led to the immediate objective of this proposal which is to test the hypothesis that endothelial cells and their biosynthetic product, endothelin-1 (ET-1), play an important luteolytic role in bovine CL function, at least in part, by mediating the effects of PGF. In the proposed experiments, we will test this hypothesis utilizing luteal cells obtained from heifers at different stages of the estrous cycle and via intraovarian administration of ET-1 and ET-1 antagonists. The specific aims are to 1) determine numbers of luteal endothelial cells, luteal content and synthesis of ET-1, and expression of ET-1 and its receptors (ETA) in luteal tissue during the estrous cycle and early pregnancy, 2) clarify the cellular mechanisms by which ET-1 inhibits progesterone production, 3) determine if ET-1 injected directly into the CL induces luteolysis and whether ET antagonist administration prevents spontaneous and PGF-induced luteal regression and 4) determine luteal secretion of ET-1 during spontaneous and PGF-induced luteolysis. The net results of these experiments should yield valuable new information on the cellular mechanisms involved in luteal regression. These results will lead to development of better methods of fertility control in the cow, improved techniques for estrous cycle synchronization and decreased losses due to embryonic mortality in all domestic species.

9703709 Physical Activity and Protein Utilization in Healthy Children
Rodriguez, N.R. **Grant 97-35207-4620**

University of Connecticut **Seed Grant**
Department of Nutritional Sciences **$49,909**
Storrs, CT 06269 **2 Years**

Current health priorities for the United States, as well as a recent Surgeon General's Report, focus on increasing physical activity and improving fitness in young children. While much is known regarding the benefits of exercise in adults, relatively little is known regarding the effects of increased physical activity on the health and nutrient needs of young boys and girls. Since protein, a nutrient required by the body, is essential for the production of muscle required to support growth in young children, it is important to determine the effects of exercise on protein use by the body in this population. This project is designed to assess the effects of physical activity on the use of protein by the body in healthy boys and girls aged 8 to 10 years. Children will participate in an 8 week study. Following a 2 week baseline period, boys and girls will begin a 6-week walking program. Measurements will be made before and after the exercise program to determine protein use by the body. In addition, food intake, physical activity, and body composition will be established for each child. This study will be one of the first to describe how exercise influences the use of protein by the body in young boys and girls and will contribute to existing information regarding the protein requirements in young children.

9703934 Ecological Significance of Frass Ejection Behavior in Lepidopteran Larvae
Weiss, M.R. **Grant 97-35311-5151**

Georgetown University **Seed Grant**
Biology Department **$50,000**
Washington, DC 20057-1229 **2 Years**

This study investigates a little-known but widespread larval behavior that may have important implications for control of lepidopteran pests. Larvae in at least seven diverse families of butterflies and moths forcibly eject frass pellets for great distances, using an anal cone that seems to have evolved for the purpose. Frass ejection behavior is closely associated with a shelter-building habit, suggesting strong selection against retention of frass in shelters. I will use *Epargyreus clarus (*Hesperiidae*),* the silver-spotted skipper, as a model system to experimentally evaluate three non-exclusive hypotheses that may explain the ecological significance of frass ejection behavior in shelter-building larvae. Briefly, these hypotheses concern 1) chemical cues for natural enemies, 2) exposure to pathogens, and 3) crowding and its consequences. Investigations of insect behavioral ecology have been important in the development of targeted approaches to pest management. Although lepidopteran larvae are major pests of agricultural crops and forest trees, we know little about the behavior of most species. Many important crop pests build leaf shelters; investigation of the functional significance of frass-ejection behavior will increase our understanding of lepidopteran larval ecology, and may help to identify a window of vulnerability for control of pestiferous shelter-building larvae.

9703554 DNA Sequencer for Avian Research
Burnside, J.; Morgan, R. **Grant 97-35208-4917**

University of Delaware **Equipment Grant**
Department of Animal and Food Sciences **$50,000**
Newark, DE 19717 **1 Year**

The Department of Animal and Food Sciences of the University of Delaware has a strong research focus in the area of poultry biology and disease. Current research programs address both applied and basic aspects of diseases such as Mareks disease, infectious bronchitis, infectious bursar disease and chicken anemia. Many of these programs have reached a stage where a more thorough understanding of the molecular structure of disease-causing microorganisms and disease processes would significantly advance progress towards development of new strategies to improve the health and safety of our flocks. In order to achieve this, we need to launch a significant effort to obtain DNA sequence information on viral genes, as well as chicken genes involved in mediating the disease process. An automated DNA sequencer would increase our capacity to generate new sequence 10-20-fold, over currently used, manually-based sequencing techniques. The identification of new genes, or genes whose mutation results in altered virulence of poultry pathogens will lead to development of more efficacious and safe methods to control disease associated with raising poultry.

9703717 Protein Prenylation in Plants
McGeady, P. **Grant 97-35106-5058**

Clark Atlanta University **Seed Grant**
Department of Chemistry **$50,000**
Atlanta, GA 30314-4358 **2 Years**

In recent years the focus of biochemical studies has shifted from the study of individual molecules such as enzymes and other proteins to the study of systems composed of these molecules. Much progress has recently been made in understanding how these systems interact to form what are known as signaling pathways in humans and in other organisms. These pathways are of great importance in normal growth and development and in the growth of tumors. Central to many of these pathways is the modification of protein molecules by small lipid molecules called isoprenoids in a process known as protein prenylation. It has been found that protein prenylation is essential for the function of many proteins. In fact, many signaling pathways become inactive in the absence of protein prenylation. While both signaling pathways and protein prenylation have been extensively studied in humans and a variety of other organisms, much less is known about these subjects in plants. It would be expected that plants, like other organisms, rely upon these pathways to carry out essential functions. Some of the possible processes that may be under the control of protein prenylation-dependant pathways are: shoot and flower development, fruit growth and ripening, and also the normal growth of the plant. We hope that by studying protein prenylation in plants we will come to a better understanding of the signaling pathways involved in these and other processes.

9703430 Metapopulation Genetic Dynamics of Weed Population Colonization and Maintenance
Gibson, J.P. **Grant 97-35311-5113**

Agnes Scott College **Seed Grant**
Department of Biology **$49,369**
Decatur, GA 30030 **2 Years**

Weeds must survive a constant cycle of population colonization, maintenance, and local extinction. One difficulty encountered by weed species is that sites suitable for their growth are spatially and temporally unpredictable. While most plant species produce a single form of fruit to locate sites, plants in some species produce fruits with two different morphologies that have different dispersal goals. Models and empirical studies have demonstrated that production of dimorphic fruits is a strategy whereby a plant produces seeds suited for growth and colonization of the distinct environments of a newly colonized site or an existing population. Using allozyme and DNA analyses, genetic characteristics will be compared between seeds that are locally dispersed versus seeds that are distantly dispersed. Mating system analysis of flowers that produce different fruits will be conducted to determine how the genetic composition of the seed pool is produced. Finally, locally and distantly dispersed seeds will be grown under different environmental conditions in order to determine whether there are also genotypic attributes of the plants associated with the success of a particular dispersal strategy. These studies are the first phase of a larger research program focusing on weed metapopulation genetic dynamics. Genetic analyses combined with competition studies will provide insights on genetic attributes of population colonization and patterns of gene movement within and among populations in weed species. The results will be useful for developing models to project movements of novel genes accidentally introduced from transgenic crop species into populations of weedy relatives.

9703944 Avoidance of Aluminum Toxicity in Legumes: Role of the Root Cap
Miyasaka, S.C. **Grant 97-35106-5060**

University of Hawaii, Manoa **Research Career Enhancement Award**
Department of Agronomy & Soil Science, Hawaii Branch Station **$56,396**
Hilo, HI 96270-4037 **1 Year**

Aluminum is a major component of soils. Under acid soil conditions, aluminum is solubilized and toxic levels can limit plant growth. Nearly half of all non-irrigated, arable lands in the world are acid, plus there are concerns about increasing soil acidity due to fertilization or acid rain. Some plants can resist the toxic effects of aluminum by release of chemicals that can bind to and detoxify aluminum. Root cap cells that separate from root tips are actively involved in exuding chemicals. Genetically engineered legume roots with known changes in root cap cells will be used to study whether these genetic manipulations have altered root sensitivity to aluminum toxicity. In addition, root cap cells of legume varieties that differ in response to aluminum will be analyzed for release of chemicals capable of detoxifying aluminum. The overall goal of this research is to improve sustainability of crop production by increasing the ability of plants to resist aluminum toxicity.

9702219 Ambrosia Beetle-plant Interactions: Influence of the Ambrosia Fungus Strain
Daehler, C.C. **Grant 97-35302-4262**

University of Hawaii, Manoa
Department of Botany
Honolulu, HI 96822

New Investigator/Strengthening Award
$180,000
3 Years

Ambrosia beetles bore into the wood of many economically important trees, inoculating the wood with an ambrosia fungus that they carry with them in a small pouch. The ambrosia fungus then grows within the bored tunnel, providing an essential food source for the beetle. In some cases, this fungus is pathogenic to the tree. This study aims to understand how genetic variation in the ambrosia fungus carried by an ambrosia beetle (the black twig borer) can influence both the severity of damage in attacked trees and the reproductive success of the beetle. Introduced to Hawaii in the 1960s, the black twig borer can cause severe damage to koa (*Acacia koa*), a fast-growing endemic tree that is prized for making high-value wood products. Previously established plots of some 3,000 koa saplings from 20 different families will be used to test for genetic variation in black twig borer resistance and variation in koa response to inoculation by different ambrosia fungus strains. Survivorship and growth of black twig borers carrying different ambrosia fungus strains will also be compared in the plots. Koa is a promising crop for planting in Hawaii's extensive abandoned sugar cane fields, and an understanding of the black twig borer-ambrosia fungus-koa interaction is needed to ensure continued successful growth of the koa wood industry in Hawaii. At the same time, this model system is expected to provide insights into how variation in an ambrosia fungus can interact with plant genetic variation to influence ambrosia beetle damage in other economically important trees.

9703743 Development of a Mimosineless Variety of *Leucaena* sp.-a Useful Fodder Legume
Hemscheidt, T.K. **Grant 97-35311-5115**

University of Hawaii, Manoa
Department of Chemistry
Honolulu, HI 96822-2275

Seed Grant
$50,000
2 Years

The tropical leguminous tree *Leucaena* sp. produces a highly nutritious and digestible protein suitable for use as cattle feed. Widespread use of this plant as fodder is limited by the presence of a toxic amino acid, mimosine, in most parts of the plant. Ingestion of this toxin in uncontrolled amounts over extended periods is detrimental to the health of foraging animals. To allow wider use of this plant as feed in subtropical agriculture, the mimosine content has to be reduced or the production of the toxin abolished entirely. This project is designed to understand the chemistry of formation of the toxin mimosine in *Leucaena* as a first step towards elimination of the genes responsible for toxin production. Initially, the plant will be supplied with a variety of compounds labeled with stable isotopes whose incorporation into the toxin will be monitored by spectroscopic methods. Analysis of the incorporation pattern will yield a biogenetic hypothesis, i.e. a proposal of how the plant synthesizes the toxin from common metabolic products. This hypothesis will next be tested in a cell-free system derived from plant seedlings to demonstrate the existence of the enzyme activities postulated in the biogenetic hypothesis. Enzymes which are specifically involved in toxin biosynthesis can eventually be used as targets for the manipulation of their expression.

9703497 Asset Mapping as an Alternative Form of Rural Economic Development
Grey, M.A. **Grant 97-35402-4885**

University of Northern Iowa
Department of Sociology, Anthropology and Criminology
Cedar Falls, IA 50614-0513

Research Career Enhancement Award
$64,900
9 months

Rural communities often seek innovative ways to encourage economic development. One alternative form of economic development strategy is asset mapping. This strategy emphasizes the identification of skills and expertise among rural community members and how these can be used to attract new economic enterprises or maintain existing jobs. This method emphasizes long-term solutions for maintaining viable rural communities rather than short-term responses to specific problems. Asset mapping also emphasizes that community members can be the most appropriate and self-sustaining force behind rural economic development rather than the more traditional institutions associated with local and state government. This research will determine the suitability of asset mapping in rural Iowa communities that have experienced recent influxes of minority newcomers. In particular, this research will determine how asset mapping can help established residents and newcomers to discover each others' special skills and talents and how these can contribute to the community's long-term economic stability. This technique may also encourage the development of a joint vision of the community's future. Doing so, the local workforce will stabilize, assuring the long-term health of local food processing and community's role in adding value to local agricultural products.

9701560 Quality, Safety Monitoring and Fault Diagnosis in Multivariable Food Processing
Cinar, A.; Balasubramaniam, V.M. **Grant 97-35503-4887**

Illinois Institute of Technology **Strengthening Award**
Chemical and Environmental Engineering Department **$160,000**
Chicago, IL 60616-3793 **3 Years**

In the growing markets for value-added food products, the quality, nutrient value, and safety of products have an important contribution in the worldwide competitiveness of U. S. agricultural and food products. For most quality and safety variables, sensors that can make direct measurements during the food processing operation are not available. Statistical process monitoring, quality control, and fault diagnosis methods provide a low-cost high-return alternative solution for maintaining high product quality and safety, and reducing quality variations. The objective of the proposed research is to develop new process monitoring, fault diagnosis and supervision techniques for food processes based on multivariate statistical theory, system theory, and artificial intelligence tools. The goal is to develop fast and accurate methods for monitoring product quality and safety, diagnosing source causes for manufacturing inferior quality or unsafe products, supervising process information assessment, and providing useful refined information to plant personnel for implementing timely corrective action. Multivariable process monitoring tools will be based on canonical variate state space modeling, principal components analysis, and projection to latent structures techniques. Fault diagnosis methods will rely on pattern recognition techniques such as hidden Markov models and time warping and on artificial intelligence tools. Supervisory information assessment and suggestions for corrective action will be carried out by a real-time knowledge-based system developed in G2 software environment. The methodology developed will be tested with two food processing operations, a high-temperature short-time (HTST) dairy pasteurization system and a fully cooked breakfast sausage process. The work will be carried out in collaboration with National Center for Food Safety and Technology (NCFST), regulatory agency, and industry. The HTST pasteurization system is a pilot plant scale unit located at the NCFST. The breakfast sausage process is a commercial production line, and data from this process will be used without interfering with process operation. The methodology and software developed would be useful in many other food processes, benefitting the food processing industries.

9701416 Molecular and Developmental Analysis of Shoot Growth of *A. thaliana*
Pickett, F.B. **Grant 97-35304-4658**

Loyola University of Chicago **New Investigator Award/Strengthening Award**
Department of Biology **$90,000**
Chicago, IL 60626 **2 Years**

The genetic regulation of the development of plant embryos residing within seeds is largely unknown. By identifying mutants that disrupt normal embryo formation in predictable ways, we have identified genes that promote normal embryogenesis when present in their wild-type, non-mutant form. The identification of the proteins encoded by these genes will provide insight into the molecular mechanisms that guide cells in the embryo from a naive state, to a state in which the cells can play appropriate roles in the formation of leaves, stems and flowers. We will identify novel embryonic genes by exposing plants to mutagenic chemical and physical agents, and by screening in their offspring for the physical manifestations of these gene mutations. In addition to our mutant screens, we have begun to produce a fate map of the embryo of *Arabidopsis*, a cruciferous plant related to broccoli, cauliflower and canola. The fate map will provide the time and location during embryonic development when cells encounter regulatory cues that cause them to participate in the formation of the seedling leaves (cotyledons) and the meristem. The meristem acts as an enduring embryo, producing new organs throughout plant development. All of the visible structures of plants, including stems, leaves and flowers, develop when naive cells in the meristem receive regulatory cues. Thus our fate mapping and genetic analysis comprise a combined approach to first characterize developmental programs in the embryo and then analyze the molecular mechanisms that organize and direct these developmental programs.

9703741 Characterization of a Resistance-breaking Strain of Turnip Crinkle Virus
Wobbe, K.K. **Grant 97-35311-5137**

Worcester Polytechnic Institute **Seed Grant**
Department of Chemistry and Biochemistry **$50,000**
Worcester, MA 01609-2280 **2 Years**

One possible route to prevention of crop loss due to infectious agents is to further understand how some plants identify and initiate defense responses to particular infectious agents, such as viruses or bacteria. This may allow manipulation of the process to broaden the spectrum of infectious agents that the plant can successfully defend itself against. The goal of the proposed research is to identify the part of a virus, turnip crinkle virus (TCV), that is recognized by the plant *Arabidopsis thaliana*. When a normal, or wild-type, TCV infects a strain of *A.thaliana*, the plant recognizes the presence of the virus and initiates a number of defensive mechanisms which result in localization of the virus to a small region of the leaf. A mutant, or variant, of TCV has

been isolated that no longer causes the defense responses on *A.thaliana*. We propose to find all of the differences between the normal and the variant strains of TCV, and then make different combinations of normal and variant TCV genetic material to determine where the difference that causes the loss of defense response is in the genetic material. Once this has been determined, we will make further changes in the normal strain to see if other changes in the same area will have a similar effect. In this manner, we hope to delineate the region of the virus that is recognized by
the plant.

9703706 The Effects of Temperature and Dietary Lipids on Growth of Channel Catfish
Seddon, W.L. **Grant 97-35208-4754**

Frostburg State University **Seed Grant**
Department of Biology **$30,407**
Frostburg, MD 21532-1099 **1 Year**

Temperature is a major environmental factor limiting the growth of poikilothermic animals, including channel catfish. Because of this, the geographical range over which catfish farming is profitable is limited to the southern states, where water temperatures are more favorable. It is possible that growth rate could be accelerated at low temperature through modifications of standard diets. Lipids, a rich source of energy in the diet, are prime candidates for research in this area. Recently, several studies have reported that medium-chain triglycerides added to standard commercial diets may benefit some fish species in terms of enhancing growth rate and lean body mass accretion. The purpose of this study is to investigate the possibility that diets supplemented with medium-chain triglycerides could enhance growth and lean body mass accretion of channel catfish at less than optimal environmental temperatures. Channel catfish will be held at 15°C or 25°C and fed either a control diet or the control diet supplemented with 6% medium-chain triglycerides or long-chain triglycerides for 70 days. Liver lipid composition, carcass lipid, ash, and protein content will be determined at the end of the feeding trial. This study will provide insight into lipid metabolism in general, as well as increasing the limited body of knowledge available on lipid metabolism as a function of environmental temperature in fish. The proposed experiments could lead to diet formulae which enhance growth at low temperature and improve quality of farm raised fish overall in terms of lean body mass.

9703498 Interaction of cAMP-and rpoS-Regulons in *Escherichia coli* O157:H7 During Substrate Accelerated Death
Byrd, J.J. **Grant 97-35207-4773**

St. Mary's College of Maryland **Research Career Enhancement Award**
Department of Biology **$50,635**
St. Mary's City, MD 20686 **1 Year**

The bacterium *Escherichia coli* 0157:H7 is currently considered a significant public health hazard which is responsible for 7,000 to 20,000 cases, 150 to 300 deaths and $230 to $600 million in medical and productivity costs each year in the United States. Transmission occurs primarily through the consumption of contaminated food (i.e., raw ground beef; apple cider; dry, fermented sausage) and water. The ability of *E. coli* 0157:H7 to survive in acidic food and its general stress tolerance is genetically regulated. These stress tolerance genes regulate over 30 proteins that aid in stress-survival. An interesting pattern identified during the characterization of this regulation in *E. coli* O157:H7 was as follows: *E. coli* grown to a point where no more organisms could grow in the flask and then inoculation into nutrient deplete conditions would die when presented with glucose. This phenomenon was previously entitled substrate accelerated death (SAD). *E. coli* O157:H7 mutants that were less likely to survive acidic conditions where also found to be more susceptible to SAD than the wild-type. In addition, SAD was found to be alleviated by the addition of the regulatory compound, cyclic AMP (cAMP) in both the mutant and wild-type. The goal of this study is to further define the role of cAMP in the starvation survival process and subsequent revival from the starvation conditions. To accomplish this goal, mutants in known regulatory systems that interact with cAMP will be studied. In addition, mutants in glycogen and trehalose (2 sugars produced by *E. coli* O157:H7 as components of the starvation survival process) synthesis will also be examined since both are regulated indirectly by cAMP. Results of this study may lead to a better understanding of the resilient properties of this pathogen and possibly lead to a novel control strategy through this accelerated death. These experiments will be completed during a sabbatical in the laboratory of Dr. Charles Kaspar at the Food Research Institute of the University of Wisconsin-Madison.

9703474 Alternative Phenolic Antioxidants for Extruded Foods
Camire, M.E. **Grant 97-35501-4602**

University of Maine **Seed Grant**
Department of Food Science and Human Nutrition **$49,316**
Orono, ME 04469-5717 **2 Years**

Extrusion cooking is used to produce a wide variety of foods - breakfast cereals, snacks, candies- and feeds. The extrusion process renders foods more susceptible to rancidity, or lipid oxidation, yet conventional methods to control oxidation have limited benefits for extruded foods. Phenolic compounds such as vanillin naturally found in foods have the potential to act as more effective antioxidants than commercial additives. An oatmeal-based breakfast cereal will be used to study the effectiveness of phenolic chemicals as antioxidants added prior to extrusion. These natural antioxidants will be studied by their chemical structure, which is similar to commercial synthetic antioxidants . Chemical and sensory evaluations of oxidation will be made six times in one year. The effects of added phenolics on color and other physical properties will also be analyzed. During the second phase of the project, selected natural phenolics will be compared with commercial strategies.

The objective of this project is to find which properties of natural phenolic compounds improve antioxidant activity in extruded foods. This project uses the extrusion process to innovatively enhance antioxidant performance. Alternate sources of food antioxidants will benefit American food manufacturers and consumers by extending shelf-life and enhancing food quality. New industries could be developed to recover these natural additives from agricultural wastes. Health risks due to cancer and heart disease may be minimized by reduction of free radicals in the food supply. Commercial application of this technology could occur within 5-10 years, since these compounds naturally exist in many foods.

9704051 Biological Feasibility of a Beta-Glucan Treatment for Lobsters
Bayer, R.C. **Grant 97-35208-4706**

University of Maine **Seed Grant**
Lobster Institute **$49,793**
Orono, ME 04469 **1 Year**

An estimated 2.5 million kg of American lobsters (*Homarus americanus*), roughly 10% of annual U.S. landings, are maintained in 65 pounds along the Maine coast. Lobsters in tidal pounds experience diseases such as gaffkemia (red tail), shell disease, ciliated protozoan disease, and vibriosis. With the exception of gaffkemia, no effective means presently exist to combat diseases, and $3 million is lost annually due to mortalities.

The immunostimulatory compounds beta-glucans have recently shown potential in preventing some diseases of fish and shrimp. This study will assess the feasibility of a beta-glucan treatment in lobsters. Experiments will test different beta-glucan doses, and means of administration. Beta-1, 3-glucans will be administered by immersion, injection, or oral route. Experiments will be conducted to determine optimal treatment doses for each mode of administration. Glucan treatment will be measured by the strength of immune responses. Treatment effectiveness will also be evaluated through challenges of treated lobsters with known disease organisms.

9701538 Relation of Myoglobin Structure and Prooxidant Activities to Fish Meat Quality
Cashon, R.E. **Grant 97-35503-4927**

University of Maine **Strengthening Award**
Department of Biochemistry, Microbiology, and Molecular Biology **$143,432**
Orono, ME 04469-5735 **3 Years**

The pigments most responsible for the bright red surface color of fish meat are oxymyoglobin and oxyhemoglobin. Changes in the coloration of both unprocessed and processed fish meat are largely due to oxidative and chemical changes in the myoglobin content. Further, myoglobin is known to interact with other components, particularly lipids, enhancing oxidative processes. Few, if any, comprehensive structure/function studies have been published comparing the myoglobins of fish species of commercial significance. Our proposed research will address this deficiency through four explicit objectives: (1) determine the primary protein sequences of a selected group of teleost fish myoglobins using PCR amplification, cDNA cloning and sequencing; (2) characterize the purified myoglobin from each of the selected fish species with respect to protein stability and prooxidant potential; (3) correlate the structural and functional data into meaningful model(s) to identify individual residues and features important to myoglobin structure and prooxidant properties; (4) integrate the biochemical/structural findings into models which describe (a) the relationship of myoglobin oxidation and meat quality in a wide variety of fish species and (b) strategies to try to intervene in the oxidation process where possible. Successful completion of these 4 objectives will provide a comprehensive basic scientific understanding of the relationship between fish myoglobin structure and its inherent peroxidase-like activity. This information is of direct relevance to both the seafood and aquaculture industries.

9703494 Investigations of Physical Properties of Biological Materials
Donahue, D.W. **Grant 97-35501-4636**

University of Maine **Equipment Grant**
Biosystems Science and Engineering Department **$48,060**
Orono, ME 04469-5710 **2 Years**

The Instron(r) materials testing system will be used to enhance the Maine Agriculture and Forestry Experiment Station's food quality research efforts, other similar research efforts and research with industry cooperators. The area of food quality research, which includes faculty and students in programs of Bio-Resource Engineering, Food Science and Human Nutrition, and Animal, Veterinary and Aquatic Sciences, has been recently extended by the appointment of this principal investigator, a food engineer, and enhanced by the affiliation with the USDA regional project NE-179: Technology and Principles for Assessing and Retaining Quality of Fruits and Vegetables. The regional project has U. S. researchers working on defining, enhancing, and maintaining the quality of fruits and vegetables.

The requested equipment will enable fulfillment of the objectives of the food quality research projects such as firmness and physical properties measurements of fresh pack Maine wild blueberries and determination of shell strength and its relationship to diets of American lobsters. These measurements will contribute to the information base on food quality and facilitate understanding how food quality can be maintained and increased. The equipment will assist in addressing important issues necessary to relate attributes of food quality to particular processing practices. The equipment will help to strengthen the team-based research efforts at the University of Maine, filling a void in knowledge needed concerning food quality. It also offers industry scientists a valuable resource for testing and improving the quality and increasing market flexibility of Maine-produced foods.

9703492 Effects of Temperature on the Growth and Metabolism of Larval and Juvenile Atlantic Cod
Hunt von Herbing, I. **Grant 97-35208-4707**

University of Maine **Seed Grant**
School of Marine Sciences **$49,989**
Orono, ME 04469 **2 Years**

This study investigates the effects of temperature on the metabolic costs of growth and activity in larval and juvenile Atlantic cod, *Gadus morhua*. Larval fish have high growth and mortality rates which decline when larvae metamorphose to juveniles. There is little information about the physiological processes that facilitate such high growth rates in fish. For example, we do not know whether high growth rates are achieved at the expense of other activities such as swimming. To study the physiological changes with growth in larval and juvenile cod, two physiological variables were chosen: aerobic scope (which represents the total energy available for all functions), and specific dynamic action (SDA), which represents the costs of feeding, digestion, and protein assimilation for growth). By comparing these two variables at different temperatures, we can determine the optimal conditions for maximal growth in larval and juvenile stages. Both aerobic scope and SDA will be determined for individual fish over a 6 month interval, using swimming respirometers and video analysis. From these measurements we can determine the relationship between the cost of growth (SDA) and growth rates at different temperatures for individual fish as they grow from the larval to the juvenile stage. These approaches will further our understanding of the ways in which growth is regulated in fast growing stages of Atlantic cod and provide the methodology to investigate the physiology of growth in other species of marine fishes important to aquaculture.

9703946 An Agricultural Systems Approach to Estimating Land Use Transitions
Plantinga, A.J. **Grant 97-35314-5121**

University of Maine **Strengthening Award**
Department of Resource Economics and Policy **$122, 900**
Orono, ME 04469-5782 **2 Years**

Land use change can have substantial impacts on environmental quality and hence the long-term viability of U.S. agriculture. Policies to limit socially undesirable land use change must recognize linkages between land use and other components of the agricultural system. In the research, we study the relationships between production and land use decisions of producers, markets for agricultural products and inputs, and soil resources. In addition, we consider how land use policies can change the economic incentives faced by producers and thereby result in land use allocations that minimize environmental impacts.

The central objective of this project is to develop a framework that allows us to simulate the effects of land use policies on land use shifts and environmental quality. Commonly-available data on land use can be used to determine net changes in land use; however, in many instances, environmental policy-makers require knowledge of the acreages of land shifting between uses. Information on land use shifts is essential since the environmental impacts of land use change typically do not “net out.” We develop a methodology for estimating the complete set of land use transitions using widely-available data from federal sources.

The methodological framework is used to study land use change in Maine and Iowa. The results are then applied to three policy problems: the design of land use regulations to limit urban sprawl (Maine), the use of zoning and other land use policies to encourage sustainable agricultural practices and minimize negative environmental impacts (Iowa), and the management of land-based carbon (Maine and Iowa). This project provides essential information to county-level zoning and agricultural program administrators and state and national policy analysts. To facilitate the transfer of information, this project is a collaborative effort between university researchers and state and federal planners and analysts. Additional beneficiaries will be targeted in efforts to disseminate the results.

9701831 Effects of Local Hospital Transitions on Rural Economic Development
Colgan, C.S.; Bird, D.C. **Grant 97-35401-4560**

University of Southern Maine **Strengthening Award**
Muskie Institute of Public Affairs **$160,000**
Portland, ME 04104-9300 **2 Years**

Using a combination of quantitative and qualitative methods, this study will examine the effects of rural hospital transitions (including closings, downsizings, conversions to other levels of care, and mergers) on rural economic development. The study will: develop a significantly improved empirical understanding of the contribution to rural economies of the health sector in general, and hospitals in particular; examine the rural economic development impact of several major federal health care financing and delivery policies; compare and contrast the experiences of a number of rural communities with local hospital transitions; and propose strategies to enable rural communities faced with hospital transitions to respond more effectively to changes in their health services and their local economies. A national Advisory Committee, comprised of recognized experts in the fields of rural economic development and health services research, will provide the project research team with overall guidance; necessary input on research questions and data acquisition; and interpretation of findings within a broader context. Dissemination routes will include Rural Development Perspectives and Rural Conditions and Trends, as well as local cooperative extension and Area Health Education Center (AHEC) agents. In addition to articles about the study, an electronic workbook will be produced and made available to local rural economic development councils and rural hospitals through the Internet web site of the Maine Rural Health Research Center.

9703718 Evaluating Indole-3-acetonitrile As a Phytoalexin of *Arabidopsis thaliana*
Tsuji, J.

Siena Heights College
Biology Department **$50,000**
Adrian, MI 49221-1796 **2 Years**

Pathogens inflict billions of dollars of damage on crop plants every year. However, despite the importance of plant diseases, our understanding of the mechanisms by which plants suppress the growth of potential pathogens is not complete. Many plants synthesize antimicrobial compounds called phytoalexins following exposure to plant pathogens. Phytoalexins are thought to suppress the growth of microorganisms and contribute to a successful defense against disease. *Arabidopsis thaliana*, an experimental plant related to cabbage, broccoli, and canola, synthesizes a phytoalexin called camalexin. Preliminary work with *Arabidopsis* suggests that indole-3-acetonitrile (IAN) may also function as a phytoalexin of *Arabidopsis*. The hypothesis that IAN is a phytoalexin of *Arabidopsis* will be tested using high performance liquid chromatography and mass spectrometry. Camalexin-deficient mutants of *Arabidopsis* will also be examined for IAN to determine whether the role of phytoalexins in the resistance response of *Arabidopsis* needs to be readdressed. In the future, genes important for the biosynthesis of IAN may be cloned and characterized for the purpose of enhancing the disease resistance of canola and other related crops.

9703445 Maize Recombinant C4-PPDK: Crystal Structure Determination and Cloning of its Regulatory Protein
Chastain, C.J.

Moorhead State University
Department of Biology **$41,815**
Moorhead, MN 56563 **2 years**

The crop plants maize, sorghum, and sugarcane possess a unique from of photosynthesis called C4 photosynthesis. This enables these species to be inherently more productive in biomass production and grain yield than other crop species, such as wheat and rice, that possess only the more conventional C3 form of photosynthesis. Research to date has implicated several enzymes which control the volume of CO_2 assimilated during C4 photosynthesis. One of these "rate limiting" enzymes is pyruvate phosphate dikinase, or PPDK. Hence, one strategy for improving yields in C4 crop species is to improve photosynthetic performance of PPDK using genetic engineering technology. We have made the first step towards this goal by cloning the PPDK gene from maize into the bacterium *E. coli*. When cloned in this bacterium, it can be selectively changed or altered using

recombinant DNA techniques. However, before this enzyme can be altered in a useful way, we need to have a detailed picture of how the enzyme is put together. We seek to do this by subjecting the enzyme to X-ray crystallographic analysis. This will yield a 3-D image of the enzyme akin to a building blueprint. This "blueprint" will provide us specific starting points for genetically altering catalytic properties of the enzyme. Another goal of this proposal seeks to clone the gene encoding PPDK regulatory protein, or RP. RP functions to activate the enzyme during the day and de-activate the enzyme at night. At present, RP is poorly understood in terms of how it can sense light and dark for activating or deactivating PPDK. By cloning its gene, it will be possible to gain such biochemical details. This information, together with the X-ray crystal structure of PPDK, will be employed for improving productivity of C4 crop species by improving the photosynthetic performance of PPDK via genetic engineering.

9703422 Cloning of Alpha-Galactosidase and Beta-Galactosidase from Avocado Fruit
Starrett, D.A.

Southeast Missouri State University
Department of Biology
Cape Girardeau, MO 63701-4799

$43,550
2 years

We propose to determine the importance of Alpha-galactosidase and Beta-galactosidase, two putative softening-related enzymes, in avocado fruit ripening, and hope to attenuate the softening and/or ripening of avocado fruit by controlling the expression of their genes.

Partial-length fragments of these genes previously cloned from ripening avocado fruit will be used to isolate full-length clones from a previously constructed avocado cDNA library. The DNA sequences of the full-length clones will be determined and the genes then converted into antisense constructs which will be used to turn the genes off in avocado fruit. Concurrently, we will continue working on a system for inserting the antisense genes into avocado tissue and regenerating whole plants. The final phase of the project will be to study the transgenic antisense plants for altered phenotypes. If as expected, these enzymes are involved in softening, or other critical aspects of ripening, then antisense fruit may show delayed or attenuated softening/ripening, and therefore extended shelf-life.

Fifty percent of avocados harvested spoil before they reach the consumer. The major problem is that many fruit soften on their way to, or in, the marketplace, which means that they are more susceptible to damage due to handling and pathogen invasion. Our long term goal is to exploit mechanisms that regulate fruit ripening and senescence to control the large postharvest losses of fruits and vegetables that occur by: reducing the energy needed to store refrigerated produce; increasing postharvest shelf-life, quality and consumer acceptance; and maintaining the inherent ability of produce to resist disease.

9701727 Nondestructive Monitoring of Hybrid Corn Possessing Genetically Modified Starch
Campbell, M.R.

Truman State University
Division of Science
Kirksville, MO 63501-4221

Grant 97-35503-4753
New Investigator/Strengthening Award
$61,894
2 Years

Most corn in the United States is used as animal feed, however, in recent years an increasing amount has been refined in order to produce various food and nonfood products. Starch, a major product from corn refining, is a raw ingredient for manufacturing many of these. Some examples include corn sweeteners, biodegradable packing materials, fuel ethanol and modified starches used in processed foods. Corn farmers in the United States directly benefit from these uses because it increases the demand for corn and the profitability of farming. To further expand the use of corn, scientists have developed hybrids with genetically modified starch. In the food industry there are several advantages in using these. For example, they do not require regulatory approval and they have fewer problems associated with consumer acceptance since they are "all natural." As the acreage of genetically modified starch hybrids increases, a major obstacle limiting their availability to industrial processors is keeping it separated from normal corn during grain transportation and storage. Those involved in handling grain would greatly benefit from a method to monitor the purity and avoid contamination. The objective of this research is to provide the grain industry with a rapid, non-destructive method to test the purity of these hybrids. We plan to investigate the use of Near-Infrared Transmittance Spectroscopy (NITS). Using numerous corn varieties we will try to calibrate the instrument so it will "recognize" hybrids with genetically different starch. Many elevators and grain processing facilities currently have NITS instruments in operation for routine testing of protein, starch and oil content. If the NITS instrument can be calibrated for starch quality characteristics from our research, instruments used in industrial settings could simply load our calibration with minimal additional expense or training.

9702007 Fluorescent Microplate Reader Uses in Agriculture Research
Ainsworth, A.J. **Grant 97-35208-4862**

Mississippi State University **Equipment Grant**
College of Veterinary Medicine **$13,035**
Mississippi State, MS 39762-9825 **1 Year**

The goal of this Equipment Grant is to purchase a modern, up-to-date fluorescent microplate reader for primary use by Mississippi State University plant and animal scientists. We have five initial users already prepared to make use of the fluorescent microplate reader who are doing research on channel catfish, swine, cattle, and chickens. The plate reader will be used to enhance the sensitivity of assays already performed in these laboratories and will also allow for the development of assays that these scientists presently can not perform. The instrument will be used to study inflammation and natural killer cell activity in catfish, ovulation in swine, bovine immunodeficiency virus, and detection of *Listeria* contamination in food products, just to name a few areas. We anticipate high demand for the use of this instrument.

9700732 Nitrogen Controls Over Tree Root Production
Friend, A.L.; Coleman, M.D. **Grant 97-35101-4338**

Mississippi State University **Strengthening Award**
Department of Forestry **$200,000**
Mississippi State, MS 39762-9681 **3 Years**

Fine roots are tremendously important to forest productivity and ecosystem health. Despite their small size (< 2 mm dia.), they consume a large fraction of biomass production, enable trees to acquire nutrients for growth, and absorb from the soil nutrients that might otherwise pollute water. Root growth is known to increase in response to soil nitrogen (N) in small patches (fertilizer bands, pockets of organic matter, etc.). Yet, paradoxically, root production has been reported to decrease with N added to a forest stand. We will attempt to resolve this conflict by testing the hypothesis that increasing plant N concentration (after fertilization) decreases the responsiveness of fine roots to small patches of soil N. Eastern cottonwood (*Populus deltoides*) was chosen as the model system for this project due to its ecological importance, rapid growth rate, and applicability of results to commercial forestry, agroforestry, and bioremediation. Greenhouse studies will test the hypothesis using split-root experiments, with detailed information collected on response dynamics and changes in tissue chemistry. Field studies will test the hypothesis by establishing a large cottonwood plantation, installing plots treated with a range of complete fertilizer amendments, and patch N-enrichments within plots. Video imaging of roots and soil core analysis will be used to quantify root responses. Rigorous experimental control and measurements of tree biomass and N accumulation will make the field study particularly useful. Future studies may use this information to improve nutritional management of short-rotation forestry, to explore its ramifications to ecological processes, and/or to explain the phenomena at a more mechanistic physiological level.

9703729 Carbon Flow and Allocation in Reproductive Shoots of Oak
Kubiske, M.E. **Grant 97-35106-5056**

Mississippi State University **Seed Grant**
Department of Forestry **$49,902**
Mississippi State, MS 39762-9681 **2 Years**

Natural re-seeding of forest trees is an important issue for foresters, but seed production of some of the most important forest trees, the oaks, is very sporadic. A large proportion of the flowers that are produced on oak trees each year, as much as 90%, never develop into viable seed. One factor responsible for poor oak seed production may be lack of available carbohydrates. Developing acorns store large amounts of carbohydrates, products of photosynthesis, from leaves. A first step in studying the effects of carbohydrate production on tree seed development is to determine the pattern of carbohydrate transport from leaves to acorns. This involves determining which specific leaves on a shoot function as carbohydrate suppliers to developing acorns, and how much, if any, carbohydrates are transported between adjacent shoots. To accomplish this, a radioactive form of carbon dioxide will be fed to photosynthesizing oak leaves and used as a tracer to follow carbohydrate transport into developing acorns. This preliminary information will allow us to design more detailed experiments in which we manipulate the environment surrounding individual tree branches, or graft flower producing buds onto oak seedlings that can easily be grown in a controlled environment.

9703553 Cultivation of Podophyllum peltatum for Podophyllotoxin Production
Moraes-Cerdeira, R.; Burandt, C.L.; Khan, I. **Grant 97-35501-4886**

The University of Mississippi **Seed Grant**
National Center for the Development of Natural Products **$ 48,475**
University, MS 38677 **2 Years**

Natural anticancer drugs derived from plants such as paclitaxel from *Taxus*, vinblastine and vincristine from *Catharanthus*, are among the most successful cancer therapies. Etoposide and teniposide are semi-synthetic drugs which are derived from podophyllotoxin, a natural compound found in *Podophyllum* species. In the United States etoposide has been used for the treatment of lung and testicular cancer, and teniposide is used to treat leukemia. Drug supply is a critical problem for treatment of any disease but more so for cancer patients who rely upon naturally derived drugs, when source availability becomes an essential issue. The commercial source of podophyllotoxin is *Podophyllum emodi* Wall from India. This plant has become an endangered species due to intensive harvest. An alternative source may be the North American species, *Podophyllum peltatum* L. To ensure future supply of podophyllotoxin, high-yielding populations have been identified and a micropropagation protocol to propagate these plants was developed. The aim of the proposed research is the establishment of a podophyllotoxin production system from U.S. sources. Selection of high-yielding podophyllotoxin plants and cultivation to enhance drug yields are the scope of this project. The success of this project will depend highly on an intensive propagation program and maintenance of selected clones. The outcome of this project will ensure drug supplies for cancer patients and furthermore introduce an alternative high-value crop for American farmers.

9703267 Sexual/Asexual Conversion of the Take-all Fungus and Its Possible Role in Natural Biological Control (Take-all Decline)
Henson, J.M. **Grant 97-35311-5112**

Montana State University **Seed Grant**
Microbiology Department **$50,000**
Bozeman, MT 59717 **2 Years**

Gaeumannomyces graminis, a filamentous fungus, causes a severe root disease of wheat called take-all disease. We isolated heavily-pigmented mutants that were similar in appearance to *Phialophora* sp., the proposed asexual state of *G. graminis.* These mutants no longer caused wheat disease and could convert back to *G. graminis* at a high frequency. Spontaneous conversion of the sexual state of the fungus to the asexual state would provide the fungus with asexual propagation and additional melanin, both useful survival mechanisms in the field. Pigments can also bind and/or exclude antimicrobics, rendering pigmented cells less susceptible to their action and our preliminary results suggests that our *Phialophora* variants are more resistant than *G. graminis* to antimicrobics produced by soil bacteria. Our overall goal is to determine whether this conversion of *G. graminis* to *Phialophora* is, in part, responsible for take-all decline, a phenomenon observed in take-all infested wheat fields whereby the disease becomes less severe after successive years of cereal monoculture. Specifically, we will monitor the generation of *Phialophora* mutants in artificially infected wheat inoculated with *G. graminis* and whether this frequency increases in the presence of co-inoculated suppressive bacteria that could select for more resistant *Phialophora*. *Phialophora* variants could in turn colonize and protect host plants from the virulent *G. graminis*, leading to take-all decline. We will also investigate the nature of the genetic alteration that occurs in *Phialophora* mutants and determine if their loss of virulence is due to pigmentation.

9703677 Equipment Grant for an Automated DNA Sequencer
Quinn, M.T.; Jutila, M.A.; Pascual, D.W.; White, M.W.;
Burgess, D.E. **Grant 97-35208-4702**

Montana State University **Equipment Grant**
Veterinary Molecular Biology **$37,552**
Bozeman, MT 59717-3610 **1 Year**

Host-pathogen interactions play a key role in infectious and inflammatory diseases of livestock. In the past several years, we have developed a departmental research program that utilizes faculty expertise in parasitology, immunology, pathology, cell biology, and molecular biology to investigate mechanisms of host-pathogen interaction in disease as well as the host defense processes used by the animal to combat such pathogens. One of the key research techniques used throughout these research projects is deoxyribonucleic acid (DNA) sequencing, and the availability of efficient nucleic acid sequencing is crucial to the timely completion of this work. Currently, all of our DNA sequencing is accomplished using manual sequencing; however, this approach is very time consuming, often leads to significant delays in the progress of the research, and is a detriment to our ability to remain competitive with other institutions that have access to state-of-the-art equipment. To meet the increasing demand for rapid, efficient, and accurate nucleic acid sequencing, we propose to purchase an automated DNA sequencing system. The availability of an automated DNA sequencer would significantly strengthen the research programs in this department, accelerate

the progress of our research programs, and enhance our current research competitiveness. Ultimately, this research may lead to the development of novel strategies and/or vaccines for enhancing ruminant host defense and, thereby, enhancing the health of these animals.

9703712 Tracking Spatial Movements of Cattle with Global Position System
Bailey, D.W. **Grant 97-35106-4945**

Montana State University **Equipment Grant**
Northern Agricultural Research Center **$35,000**
Havre, MT 59501-9603 **1 Years**

The requested equipment is a livestock tracking system that uses the global positioning system (GPS) and can continuously record the location of free-ranging livestock on rangeland. This tracking system consists of 16 GPS receivers, antennas and data storage devices, which will be incorporated into 16 collars and placed on the necks of cattle. Readings from a stationary GPS receiver will be used to increase the accuracy to within three meters so that the animal's path across the landscape can be recorded. Uses for the tracking system vary, but all involve analyses of livestock movements. The GPS-detected movements of livestock will be compared to model predictions. The tracking system will also be used to observe and quantify changes in livestock grazing patterns when selected management changes are implemented. Strategic placement of supplement and salt will be evaluated as tools to lure animals away from sensitive areas and to under-utilized rangeland. The equipment will be used to evaluate if forage utilization patterns can be improved by culling animals that only graze in localized areas and do not use under-utilized areas. Animal foraging patterns will also be observed to determine if some cattle breeds use rugged topography more than others. With this information, innovative management techniques can be developed that prevent concentrated grazing and watershed degradation.

9703685 Enhancing Wheat Grain Quality Through Continuous Grain Protein Sensing and Site-Specific Nitrogen Fertilization
Long, D.S. **Grant 97-35501-4634**

Montana State University **Seed Grant**
Northern Agricultural Research Center **$49,578**
Havre, MT 59501 **2 Years**

Demand for high protein wheat is rising, especially in all developing economies that can afford to pay extra for the milling and baking qualities of this quality grain. The U.S. wheat industry is positioning to meet this opportunity by demonstrating its reliability as a supplier of premium-quality wheat and wheat products. This study is being conducted to determine whether the output of high protein wheat can be improved through a variable rate nitrogen fertilization strategy that uses information from on-the-go sensing of grain yield and protein content at harvest. The role of soil nitrogen, soil water, and topography in determining spatial patterns in wheat yield and protein content is also being investigated. The approach being taken uses new grain protein sensing technology to derive detailed maps of nitrogen fertility requirements within fields. The rationale is that crop growth reflects fertility conditions in the soil profile, and grain protein is a good indicator of soil nitrogen levels. Based on quantifiable relationships between nitrogen fertility and grain protein, a geographic information system can be used to mathematically combine the yield and protein data to produce composite maps of site-specific nitrogen fertilizer recommendations. This strategy promises to improve the ability to identify nitrogen deficient sites within fields at much greater detail and lower cost than is possible with conventional soil sampling. This improved capability will enhance the protein output and boost profitability.

9704060 Analysis of Rhizosphere Carbon of Native and Invasive Plant Species
Deluca, T.H.; Kiely, D.E. **Grant 97-35106-5147**

University of Montana **Equipment Grant**
School of Forestry **$15,000**
Missoula, MT 59812 **1 Years**

Plants are known to leak up to 40% of their total carbon into the rooting zone via a process known as root exudation. Innumerable processes in plant ecology are dependent upon root exudation and the influence that exudation has upon the chemistry of the rooting zone (rhizosphere). There is, however, no suitable means of studying root exudates *in-situ* (non-destructive measurement under natural field conditions). To date, root exudates have been studied under artificial laboratory conditions which do not adequately reflect the stresses of the natural environment. Our work aims to break the dependence upon artificial rooting conditions for root exudate studies by using modern resin technology. We have introduced a novel technique for the extraction of root exudates and other rhizosphere compounds in which non-ionic carbonaceous resin capsules are placed in the rooting zone of target plants. The resins sorb various compounds which can then be identified in the laboratory. Such technique may allow for the extraction and analysis of important plant-microorganism signals called flavonoids. We will analyze the rhizosphere

extracts using high performance liquid chromatography (HPLC) using a scanning ultraviolet light detector called a photo-diode array (PDA) detector purchased with assistance from the USDA. Using this equipment in combination with other analytic techniques we can effectively identify the character of these compounds. Once we have identified plant signals that are specific to invasive weeds such as knapweed, we can evaluate how these compounds influence the competitive abilities of invasive plants and thus target means of reestablishing native plant species.

9700735 Quantifying an Ecosystem Perturbation: Forests, Mycorrhizae, and Red-Backed Voles
Mills, L.S. **Grant 97-35101-4355**

University of Montana **New Investigator/Strengthening Award**
Wildlife Biology Program **$120,000**
Missoula, MT 59812 **2 Years**

Forest ecosystems have received special attention in the Pacific Northwest since President Clinton convened a special scientific panel to evaluate how management will affect forests and wildlife. One of the most crucial biotic components of Northwest forest ecosystems involves the dynamics of red-backed voles, which are a primary dispersal vector for the fruiting bodies of mycorrhizal fungi (truffles). Mycorrhizae are, in turn, essential for tree regeneration following harvest. Previous work has shown that California red-backed voles are infrequent near edges of forest remnants and absent from the clearcuts surrounding remnants in SW Oregon, but positively associated with truffles and decaying logs within the remnants. At the same time, truffles are lacking from clearcuts, most likely to be found under logs, and infrequent on the edges of forest remnants. The proposed work will fill in two gaps critical to forest sustainability. First, I will evaluate whether the striking demonstrations of negative edge effects and isolation for red-backed voles in 1990/1991 still hold nearly a decade later. Second, I will use large, replicated trapping grids to assess whether the observed negative edge effects translate into decreased birth and survival rates for red-backed voles in forest interiors relative to those on the edge, implying a demographic "sink." Such information will not only provide insight into demographic feedback between forest system perturbation and the persistence of red-backed voles, but it will also help establish protocols for long-term monitoring a species that is pivotal in Northwest forest ecosystems.

9703721 Replacement of Fire-maintained Ponderosa Pine by Douglas-fir: The Consequences for Stand Water Cycles
Sala, A. **Grant 97-35106-5061**

University of Montana **Seed Grant**
Division of Biological Sciences **$50,000**
Missoula, MT 59812 **2 Years**

Since the early 1900's, fire exclusion and livestock grazing in the interior northwestern United States have favored the replacement of open ponderosa pine (*Pinus ponderosa*) stands by dense stands of Douglas-fir(*Pseudotsuga menziesii* var. *glauca*). Ecological consequences of this successional replacement include alteration of water, carbon and nitrogen cycles. Management consequences include increased fire hazard, increased susceptibility to pathogens and decreased forest health. Here, we propose to test the working hypothesis that increases in stand density, canopy cover, and amount of foliage on a ground area basis associated with the successional replacement of ponderosa pine by Douglas-fir results in increased stand-level water use, reduced soil water availability and increased tree water stress. Measurements will be conducted in three comparable stands: a fire-maintained ponderosa pine stand, a mixed stand with ponderosa pine and Douglas-fir and a fire-excluded stand where Douglas-fir has become dominant. For each species and stand we will assess the degree to which trees are physiologically stressed by measuring water status, water loss by transpiration, and photosynthesis. We will also quantify water use by whole trees by measuring sap flow in main trunks. Stand-level water use will be estimated from these measurements and compared to soil water availability. Our long term goals are to 1) evaluate stand- and landscape-level changes of the water, carbon and nitrogen cycles resulting from the replacement of ponderosa pine by Douglas-fir and 2) assess the implications of these ecological shifts on forest productivity and health.

9704019 Purchase of a Near Infrared Spectrometer
Eckhoff, J.L. **Grant 97-35311-5149**

Montana State University **Equipment Grant**
Eastern Agricultural Research Center **$26,600**
Sidney, MT 59270 **1 Year**

The purpose of this equipment grant is the acquisition of a near infrared spectrometer (NIR). An NIR is a versatile piece of equipment that can be used for many types of research. Current projects for which this instrument will be used include evaluation of small grain, forage, and safflower. Small grain samples will be evaluated for protein content, providing information to the breeders for parental and experimental selection, and information to area producers on varietal selection. Alfalfa varieties and

other forage species will be evaluated for protein content and forage quality, to aid researchers and growers. Safflower samples will be evaluated for meal protein and fiber content to select varieties with high feed value. Several new projects will be initiated or enhanced by the purchase of the NIR. A durum improvement project for Montana and North Dakota is under development. The NIR will be used to evaluate protein content, color, and other quality components for selection of parental and experimental lines. Fertilizer N use and best management practices of irrigated and dryland small grain will be evaluated in par by analyzing grain and straw protein content. Production of vegetable crops in this area is under investigation. The NIR will be used to measure quality components of these crops, including sugar and fiber content. Data from all projects will be available for distribution to agricultural producers.

9703440 Population Dynamics and Activity of Denitrifying Bacteria
Murray, R.E. **Grant 97-35106-4801**

Appalachian State University **Research Career Enhancement Award**
Department of Biology. **$68,187**
Boone, NC 28608 **1 Year**

Nitrogen is the mineral element most commonly limiting plant growth in terrestrial, marine, and agricultural ecosystems. Denitrification is the major mechanism by which nitrogen in soil and water is returned to the atmosphere in the form of nitrogen gas. Measurements of nitrogen gas loss from soil are often highly variable and nitrogen gas loss correlates poorly with both the synthesis of denitrifying enzymes and the growth of denitrifying bacteria. The poor correlation between nitrogen gas loss and denitrifier population dynamics could be caused by problems with the existing standard measuring techniques which may underestimate the numbers and activity of denitrifying bacteria and/or the difficulties of sampling bacteria which are not evenly distributed in soil. The goal of this project is to determine the causes of the poor correlation observed in field studies between nitrogen gas loss from soil, denitrifying enzyme activity, and the number of denitrifying bacteria. This information is needed to develop an understanding of how ecosystem level measurements of nitrogen loss are coupled to the dynamics of denitrifier population size, activity, and distribution. The results of the project will provide new insights into the cycling of nitrogen in terrestrial ecosystems, the fate of nitrogen fertilizers in agricultural systems, and the production of nitrogen oxide gasses which contribute to the greenhouse effect and to the destruction of the stratospheric ozone layer.

9704020 A Transgenic Reporter System in *Drosophila* for Identifying Novel Insecticides
Henrich, V.C. **Grant 97-35311-5138**

University of North Carolina, Greensboro **Seed Grant**
Department of Biology **$50,000**
Greensboro, NC 27412-5001 **2 Years**

Insect damage is a major cause of crop economic loss. Most traditional pesticides are neurotoxins. New insecticides are being sought which act by different modes of action since insect populations develop resistance to any single insecticide, including the popular BT toxin produced by genetically-engineered crops. The primary objective of this proposal is to develop genetically-engineered strains of the fruit fly, *Drosophila*, which will allow for the direct visual observation of steroid hormone responses in developing larvae. Normally, insect steroids trigger the developmental changes during feeding larval stages and metamorphosis that are necessary for survival. However, monitoring hormonal responses typically has required the use of sophisticated molecular techniques. The ability to observe hormonal responses visually will allow fly larvae to be tested with a variety of chemical compounds and plant extracts for their ability to perturb any aspect of steroid synthesis, response, or metabolism. This bioassay will ultimately lead to the identification of specific plant compounds that act as insecticides or antifeedants.

9703740 Genetic Analysis of Tip Moth Susceptibility in Slash and Loblolly Pines
Highsmith, M.T. **Grant 97-35311-5155**

Shaw University **Seed Grant**
Division of Science and Technology **$50,000.00**
Raleigh, NC 27601-2341 **2 Years**

The pine shoot tip moth (*Rhyacionia* sp.) damages pine (*Pinus* sp.) seedlings worldwide and is a major pest in commercial pine plantations in the southeastern U.S. The most economically significant tip moth damage in the southeastern U.S. is due to the Nantucket tip moth on loblolly pine, a commercially important tree. The female tip moth deposits eggs on the shoot tips of young pine trees (< 5 years old). The developing larvae kill the shoot tips but rarely cause mortality of the whole tree. The long-term impact of tip moth damage is approximately a 28-30% reduction in wood volume after 20 years. Slash is a commercially important pine that is highly resistant to tip moth attack. Female tip moths actively choose loblolly pine seedlings in mixed plantings with slash pine. This study will use genomic mapping and molecular markers to examine the genetic basis of

susceptibility to tip moth damage using families of slash:lob F1 hybrids and F2 hybrid families from backcrosses of the slash:lob F1 hybrids and the slash parent. The backcross progeny should segregate for resistance. The slash:lob Fl hybrids will be used to examine the mode of inheritance to tip moth damage. This research could help scientists and agriculturalists better understand tree-insect interactions. Such knowledge is fundamental for improving the quality, productivity and sustainability of natural populations of forest trees and to accelerate the development of genetically superior trees that are more resistant to insect damage.

9703466 Handling Equipment for Bison Nutrition Research
Anderson, V.L. **Grant 97-35208-4722**

North Dakota State University **Equipment Grant**
Carrington Research Extension Center **$12,390**
Carrington, ND 58421-0219 **1 Year**

Commercial bison (American Buffalo or *Bison bison*) production is a new animal agriculture enterprise that is growing rapidly, especially in the Northern Plains region where bison are more adapted to the climate than domesticated ruminants. A new research program in bison is being developed at North Dakota State University's Carrington Research Extension Center to gain basic and practical knowledge in the area of bison nutrition and metabolism. The intent of this research program is to incorporate the natural strengths of bison into commercial production scenarios. The objectives for this long term research program are: (1) determine nutrient requirements for bison; (2) evaluated methods that enhance digestion of feeds and forages; (3) investigate metabolism of therapeutic agents; (4) evaluate effects of bison nutrition and management on carcass traits and meat nutrient content; and (5) develop economic information on bison production. Bison are wild animals and experience severe stress when confined or separated. Conducting bison research requires specially designed, commercially available sorting and handling equipment for restraining animals. The equipment components include a squeeze chute with crash gate and scale, palpation cage, alley segments, blocking gates, crowding tub, catwalks, loading chute, and gates and panels for loading/unloading, sorting, holding, and feeding bison. This specialized equipment will preclude injury to the animals and their handlers, yet allow timely and accurate treatment, care, and sample collection from individual and groups of animals.

9703556 Visceral Protein Metabolism: Contribution from Arterial and Luminal Supply
Caton, J.S. **Grant 97-35208-5100**

North Dakota State University **Research Career Enhancement Award**
Animal and Range Sciences Department **$65,010**
Fargo, ND 58105-5727 **1 Year**

The primary long term career goal associated with this sabbatical project is to continue developing a research program in nutritional physiology. Developing and maintaining a strong team approach in nutritional physiology research and improving quality of instruction and graduate programs are also long term career goals. Focus of the research is in the area of metabolism by visceral organs. Specific training goals associated with the project include learning techniques in animal preparation and stable isotope applications. The project will develop familiarity with newly acquired techniques in pregnant and lactating cows, expand the understanding of visceral amino acid metabolism, and provide exposure to new approaches and areas of nutritional physiology research. The specific research project will evaluate where amino acids used by the intestinal tissues originate (from the intestinal lumen or from circulating blood). Cows will be used for the study because they contribute significantly to the agriculture economy of the United States and potential exists for improving whole animal response through enhanced efficiency of visceral metabolism. Mentors and institutions include Dr. C. K. Reynolds from University of Reading, UK and Dr. John MacRae of the Rowett Research Institute, UK. The project will couple the expertise of these scientists into a single cooperative effort, resulting in a sabbatical project that will optimize time and resources spent. As a result of the project, research programs will be enhanced through a greater understanding of visceral metabolism and application of new techniques to a wide array of nutritional and physiological questions. Expertise gained will be used for accomplishing project and long term career goals.

9703536 Acquisition of an HPLC System
Hadley, M. **Grant 97-35207-4775**

North Dakota State University **Equipment Grant**
Department of Food and Nutrition **$25,612**
Fargo, ND 58105-5057 **1 Year**

Potato peel, a waste product of the food industry, contains compounds that may be used as food antioxidants. Many of the synthetic antioxidants available to the food industry are being questioned as to their safety. The peel may also contain compounds that could be used as pesticides for some crops. These compounds will be quantified from peels from several varieties of potato to determine the feasibility of their extraction.

Potato peel may also contain compounds called lignans that have been shown to reduce the risk of certain cancers. Potato peel will be investigated to determine if lignans are present and at what concentration. Barley and flaxseed contain fibers, beta-glucans and mucilage, respectively, that have characteristics similar to some of the compounds used by the food industry as stabilizers. The structure and chemical composition of molecular weight fractions of the fibers of flaxseed and barley will be investigated. Flaxseed and barley contain antioxidants which have been associated with cholesterol reduction, especially LDL-cholesterol. Concentrations of these antioxidants in different varieties of flaxseed and barley will be determined.

Anthocyanins, a complex group of natural pigments found in a variety of red and blue fruits and vegetables (i.e., apples and eggplant), may prove to be food colorants which would be of benefit to the food industry as the synthetic colorants now used are under scrutiny from a safety perspective. Elucidation of the components of anthocyanins isolated from various sources will be studied for their potential as food colorants.

9703489 Capillary Electrophoresis of Wheat Proteins in Relation to Breadmaking Quality
Khan, K. **Grant 97-35501-4639**

North Dakota State University **Equipment Grant**
Department of Cereal Science **$25,250**
Fargo, ND 58105 **1 Year**

Capillary Electrophoresis (CE) is a relatively new biochemical technique that offers a great deal of potential for researchers involved in cereal protein research. Because CE can complement the polyacrylamide gel electrophoresis (PAGE) and sodium dodecyl sulfate (SDS) PAGE as capillary gel electrophoresis (CGE), a great deal more information can be derived on the structure/function relationship of the gluten proteins. The advantages of CE and CGE over PAGE and SDS - PAGE are greater sensitivity, better resolution, no staining/destaining for detection of proteins, immediate quantitation through computer interphasing and detection via UV/visible, continuous spectra and also fluorescence analysis option. First, CE and CGE would be useful for wheat cultivar identification which is very important in cultivar development, trade and commerce. Second, analysis of protein fractions during the breadmaking process from techniques such as reversed phase - high performance liquid chromatography (RP-HPLC) by CE and CGE and vice versa, would provide useful physicochemical and structural information on the gluten proteins. This information would enhance our understanding of the functionality of the gluten proteins in the breadmaking process. This, in turn, would enable cereal chemists and plant breeders to screen for wheat cultivars with good breadmaking quality in a cultivar development program such as at North Dakota State University.

9703461 Equipment Enhancement of Animal Health Research Facilities
Nolan, L.K.; Robinson, M.; Uorne, S.M.; Dyer, N.W.; Rust, L.; White, D.G. **Grant 97-35208-4719**

North Dakota State University **Equipment Grant**
Department of Veterinary & Microbiological Sciences **$49,750**
Fargo, ND 58105 **1 Year**

We plan to purchase a benchtop flow cytometer to enhance the animal health research facilities in the Department of Veterinary and Microbiological Sciences at North Dakota State University. This instrument will be one of only two flow cytometers in North Dakota with the other instrument owned by a local hospital and devoted to clinical medicine. In contrast, the instrument we will purchase will be used for research purposes only. Flow cytometry is a powerful research tool which is increasingly recognized as standard equipment in research facilities. It allows multiple measures to be made of individual cells with great rapidity and objectivity. Although it is likely that this instrument will have many users from various campuses throughout the State, it will primarily be used to support the principal investigator's research projects. Although these projects are diverse and include studies of virulence mechanisms of *Escherichia coli,* immunity to chronic hookworm infections, intracellular survivability of *Salmonella*, diagnostic veterinary medicine, regulation of *Pseudomonas* virulence genes, and antibiotic resistance among *Salmonella and E. coli* of animals, they are all united by the common goal of improving animal health and promoting the sustainability of United States agriculture. Access to a flow cytometer on-site will greatly improve the research infrastructure of our department, university, and state and will enhance our competitiveness for future funding.

9701956 *emb10*: a Gene with Diverse Roles in Maize Embryogenesis
Clark, J.K. **Grant 97-35304-4691**

University of North Dakota **Strengthening Award**
Department of Biology **$90,000**
Grand Forks, ND 58202-9019 **2 Years**

A mature maize embryo consists of an embryonic plant surrounded by a large seed leaf, the scutellum. Mutant *emb10* embryos are frequently mispositioned within the kernel, their scutella fail to expand, and the embryonic mesocotyl, a specialized region of the embryonic shoot that is important during seedling germination, is stunted. These and other morphological abnormalities

suggest that the *emb10* gene may be involved in determining cell shape and the direction of cell division. The goal of this project is to understand the nature of the *emb10* gene and its role in maize embryo development. The course of abnormal embryogenesis in mutant embryos will be studied in sectioned materials in order to infer (by contrast) the role of the normal gene. The *emb10* gene will be cloned and its sequence will be compared with sequence databases in order to determine whether *emb10* corresponds to other genes of known function. Crosses will be made with chromosome translocation stocks and genetic markers which will enhance the effectiveness of the developmental and molecular analysis. This project will add to our knowledge of fundamental cellular mechanisms of plant development. It will provide insight into the genetic regulation of the process of embryogenesis. And since embryonic mesocotyl differentiation is a taxonomically important trait in the grasses while seedling mesocotyl extension is an agronomically important trait in maize, rice and wheat, this project will set the stage for future comparative studies of *emb10* in other cereal species.

9703679 Direct Determination of Diamine and Polyamine
Dobberpuhl, D.A.; Thomas, L.L. **Grant 97-35501-4588**

Creighton University **Seed Grant**
Department of Chemistry **$50,000**
Omaha, NE 68178-0104 **2 Years**

Elevated concentrations of specific polyamines such as histamine, agmatine, putrescine, and cadavarine are reliable indicators of putrefaction in many foods. These same polyamines also can cause severe allergic reactions in sensitive individuals. Therefore, the ability to accurately determine the concentrations of polyamines in grains, meat, and especially seafood is invaluable in assessing the overall quality of these products. Typical methods for the determination of aliphatic diamines and polyamines rely on high performance liquid chromatography with photometric detection. However, the use of photometric detection is made difficult because aliphatic diamines and polyamines have no natural chromosphere, and thus must be chemically modified (derivatized) with a photometrically-active adduct. The derivatization procedure can be laborious and problematic. Thus, there is a great need for a method that provides accurate, sensitive, and reproducible detection of these compounds with a minimum of sample manipulation. The focus of this proposal is the development of pulsed electrochemical detection (PED) methodology for diamines and polyamines separated by high performance liquid and/or ion chromatography. Because PED allows for the continuous and direct detection of aliphatic compounds without pre- or post-column derivatization, diamines and polyamines may be determined with a minimum of sample preparation. The objective of the proposed research is to devise a simple, direct, and broad-based analytical method for measuring diamine and polyamine concentrations in biological samples with demonstrated applications to fish, meats, and other foodstuffs.

9703496 Monocyte Chemoattractant Protein-1 in the Bovine Corpus Luteum
Townson, D.H. **Grant 97-35208-4705**

University of New Hampshire **Seed Grant**
Department of Animal and Nutritional Sciences **$50,000**
Durham, NH 03824-3590 **2 Years**

In cattle, the corpus luteum is a structure that forms on the ovary following ovulation and is essential for the maintenance of pregnancy. A unique characteristic of the corpus luteum, however, is its relatively short-lived existence in the non-pregnant animal. That is, in the absence of pregnancy, or in instances of early embryonic death, the corpus luteum undergoes spontaneous regression. In many species, including the cow, immune cells (e.g., monocytes/macrophages) infiltrate the corpus luteum and are suspected to play an integral role in regression. Yet the mechanisms responsible for the rapid recruitment of these immune cells into the corpus luteum remain unknown. In this study, we propose that a protein known as monocyte chemoattractant protein-1 (MCP-1) initiates monocyte/macrophage recruitment into the cow corpus luteum during regression. MCP-1 is known to attract monocytes/macrophages to sites of inflammation and immune response, and may have a similar role in regression of the corpus luteum. The aims of this proposal are to investigate whether MCP- 1 is expressed in the corpus luteum of the cow, and to determine whether there is an increase in MCP- 1 expression associated with monocyte/macrophage accumulation during luteal regression. The results of these experiments are expected to provide insight to macrophage recruitment during regression of the cow corpus luteum. The long-term goal of this work is to provide new information about the interactions between immune cells and the corpus luteum, and whether manipulation of the local immune response results in an alteration of fertility.

9703537 Spectrophotometer for Xanthan Gum Research
Harcum, S.W. **Grant 97-35501-4638**

New Mexico State University **Equipment Grant**
Department of Chemical Engineering **$11,270**
Las Cruces, NM 88003-0001 **1 Year**

Xanthan gum is a polymer produced by the bacteria *Xanthomonas campestris* and is used as a thickener, emulsifier, and stabilizer in the food industry. Food-grade xanthan gum is also used to enhance oil recovery, although the stringent purity standards required for food-grade xanthan gum are not required. Preliminary data from our laboratory suggests that xanthan gum can be manufactured inexpensively from waste agricultural products for non-food grade uses, such as drilling fluid viscosifers. To enhance this research program, as well as improve the research infrastructure at New Mexico State University, a state-of-the art UV/VIS spectrophotometer will be purchased by this grant. The UV/VIS spectrophotometer will measure and characterize *X. campestris* fermentations utilizing agricultural waste products, such as waste sugar beet pulp, pecan shells, waste whey, and chili pepper waste, as a carbon source. Understanding the degradation mechanism is crucial to improving the process. This instrument is essential for fundamental research including enzyme kinetics, gel scans, wavelength scans, DNA/RNA/Protein determination, colorimetric assays, protein purification and automated, multiple sample analysis. Other ongoing research projects that will benefit from the UV/VIS spectrophotometer are the bioremediation of acid mine drainage by algal biomass, stress response of recombinant *Escherichia coli*, and the effect of fermentation conditions on the glycosylation of recombinant proteins. As demonstrated by our current research, using agricultural waste products for xanthan gum production has the potential to add value to the waste, reduce the volume of waste that is disposed, and create a source of low cost, non-food grade xanthan gum.

9701366 RbcS mRNA Translation and Stability in *Chlamydomonas*
Baker, E.J. **Grant 97-35301-4816**

University of Nevada, Reno **Strengthening Award**
Department of Biology **$100,000**
Reno, NV 89557-0015 **2 Years**

Chlamydomonas reinhardtii, a unicellular green alga, is an excellent model system for the study of a variety of areas of basic cell biology and biochemistry, particularly photosynthesis. The ability to genetically alter both the chloroplast and nuclear genomes of this organism has allowed powerful analyses of gene function not yet possible in higher plants. In order to fully live up to its potential as a model organism, studies addressing the fundamental molecular biology of gene expression must keep pace with genetic analysis. Control of the process of translation (protein synthesis) is a key area for investigation. The amounts of specific proteins synthesized can be controlled by intrinsic differences in the abilities of different messenger RNAs (mRNAs) to be translated, and by differences in the stabilities (lifetimes) of the mRNAs serving as templates for translation. The molecular bases for these differences are not well understood. The major project seeks to understand the basis for the striking translational inefficiency of an mRNA encoding a protein subunit of the major chloroplast enzyme, ribulose bisphosphate carboxylase, RbcS2. We propose to determine which nucleotide sequences are critical for its translational inactivity by using recombinant DNA techniques to alter RbcS2 gene sequences to produce modified mRNAs *in vivo*. We have also determined that the stability of RbcS2 mRNAs can be altered by growth in different carbon sources. The second project seeks to understand the molecular basis for the carbon source-regulated stability of this mRNA and its possible relationship to translational efficiency.

9702889 Effects of Exploitation Rates on Coyote Population Ecology in Agroecosystems
Berger, J.; Gompper, M.E. **Grant 97-35316-5118**

University of Nevada, Reno **Strengthening Award**
Department of Environmental and Resource Sciences **$100,000**
Reno, NV 89512-0013 **2 Years**

In the western US, annual livestock losses due to coyotes are over $4 million and more than 97,000 coyotes/yr are killed at a cost approaching $20 million/yr. However, a largely urban population questions the need for coyote control, highlighting the need to base management decisions on sound science. Many aspects of the population biology of coyotes are density-dependent. That is, as the rate at which coyotes are removed from a population increases, the ecology of the surviving population changes. For example, removing territorial females results in increased reproduction and decreased natural mortality among surviving individuals. Thus, indiscriminate predator control programs may aggravate livestock losses if survivors breed earlier, live longer, and have larger litters. Although other aspects of the biology of coyote populations may be similarly influenced by predator control, this topic lacks empirical attention. Consequently, little is known about how predator control programs influence coyote population age structure, dispersal and recruitment rates, spatial distributions, pack sizes, and dietary habits, and how these variables in turn influence the success of the control program. We will examine these issues in coyotes occupying rangelands of the Great Basin Desert that experience a continuum of control (areas of heavy exploitation and areas of no control). Results of

the study will be immediately useful for minimizing the impacts of predators on livestock by better justifying the time, effort, costs, and strategies of predator control operations.

9703468 Acquisition of a Flow Cytometer
Garner, D.L. **Grant 97-35208-4739**

University of Nevada, Reno **Equipment Grant**
School of Veterinary Medicine **$50,000**
Reno, NV 89857-0035 **1 Year**

The overall goal is to further develop the research infrastructure at the University of Nevada, Reno so that researchers can become more competitive for future funding as well as move into new research areas. A bench top flow cytometer with rapid sample processing and cell sorting capabilities is to be purchased. Flow cytometry is a powerful research tool in the life sciences. Single cells in a population are measured rapidly (l,000 cells per sec.) and objectively with non-biased instrumentation. Several characteristics can be measured for each cell allowing determination of the relationships among the various attributes of the cells. With a sorting option, subsets of cells within a population of cells can be physically sorted out for further analyzes. Such an instrument is capable of very rapid measurements in the range of 1-3 samples per min. The research samples will have a wide range of origin related to agricultural and environmental interests. These include livestock sperm, plant, animal, microbial and algal cells. Five specific projects of five principal investigators will utilize this equipment initially: Project 1-Cryopreserved sperm organelle function and fertility; Project 2-Labeled serine protease inhibitors as probes for activatable sperm acrosin; Project 3-Relationship of the viable leukocytes in colostrum and milk to mastitis incidence in range ewes; Project 4- Dietary fat and the treatment of human mammary carcinoma; and Project 5-Relationship of DNA damage to long-term net primary production (NPP) in the green microalgae *Chlamydomonas reinhardtii*.

9704022 The Nature of Potyvirus Resistance Conferred by the *I* Gene of Bean
Collmer, C.W. **Grant 97-35311-4822**

Wells College **Research Career Enhancement Award**
Department of Biological and Chemical Sciences **$47,718**
Aurora, NY 13026-0500 **1 Year**

The long term goal of this research project is to understand the nature of the resistance to potyviruses conferred by the *I* gene of the common bean. The study of this gene(s), which may comprise a cluster of related genes and which confers resistance to a number of different potyviruses, is important for several reasons. 1) Potyviruses are the largest group of plant viruses; they can infect most crop species, and they cause serious economic losses worldwide. 2) The generation and use of resistance in plant breeding programs is the most important viral control strategy in sustainable agriculture. 3) Resistance genes that confer resistance to more than one potyvirus offer substantial advantage for plant breeding programs. Despite the well-acknowledged importance of the *I* gene to bean production world-wide, little is known about how it successfully stops some potyviruses and fails to stop others, often with devastating consequences for the plant in the latter case. The objectives of this sabbatical project are to learn, and then apply, sensitive molecular and cellular biology tools that allow visualization of early events in the interaction between different potyviruses and bean tissue with and without the *I* gene. In addition, the isolated coat protein from resisted potyviruses will be tested directly to see whether it is the elicitor of the successful resistance response in *I* gene-containing bean tissue. Understanding the specific interactants, and conditions, that set off the resistance response should inform decisions about possible wider deployment of the *I* gene in plant breeding programs.

9703734 Regulatory Sequences of Plant Protease Genes
Wilson, K.A.; Tan-Wilson, A.L. **Grant 97-35311-5117**

State University of New York, Binghamton **Seed Grant**
Department of Biological Sciences **$50,000**
Binghamton, NY 13902-6000 **2 Years**

Germination of the seed is a crucial period for the successful establishment of a crop plant. One key process in this period of the plant's life is the degradation of the seed storage proteins to amino acids to provide nutrients for seedling growth. Four enzymes have been identified to be involved in this mobilization in the mung bean (*Vigna radiata*) - two endopeptidases (Cys-EP and proteinase F), and two carboxypeptidases (Cpase I and II). Our main interest is the elucidation of the mechanisms controlling the expression of the protease genes at the different stages of the plant's life cycle. In many cases the expression of a gene (e.g., the production of the enzyme coded for by that gene) has been shown to be controlled by DNA sequences flanking the DNA coding for the protein. We will clone the genes coding for the mung bean proteases, and determine the nucleotide sequences of these genes. The sequences flanking both sides of the protein structure-coding sequence will be examined for possible regulatory sequences, based on previously identified regulatory sequences in other genes, repeated sequence motifs, etc. We will also

examine two other plants, *Arabidopsis thaliana* and *Nicotiana tobacum* for similar genes, and determine if these genes, if present, are expressed in a manner similar to that seen in the mung bean. Both *Arabidopsis* and *Nicotiana* are readily manipulated genetically, allowing us to in the future study protease gene regulation using a number of techniques (such as stable transformation) not available with the mung bean.

9704059 Application of Force Microscopy to the Study of Plant Tissue Morphologies
Batteas, J.D.; Stark, R.E. **Grant 97-351106-4800**

The City University of New York, College of Staten Island **Seed Grant**
Department of Chemistry **$50,000**
Staten Island, NY 10314-6600 **2 Years**

The cuticular layers at the surfaces of the leaves and fruits of higher plants play an important role both as a protective covering as well as a barrier for controlling surface wetting and the diffusion of molecules into the plant's tissues. This barrier also prevents water loss and provides protection from pathogenic and chemical attack. The ability of the cuticular barrier to function properly is highly dependent upon its chemical composition and surface morphology. For example, fungal infection is believed to be sensitive to the plant's surface topography, whereby cracks in the surface can enhance pathogenic destruction. Such cracking of the cuticle is believed to be dependent upon environmental factors such as temperature (for example thermal shocks associated with heat waves and frosts) and the degree of tissue hydration. The formation of cracks in the cuticle will also be dependent on the degree of elasticity within these surface layers. Until recently the topographic and mechanical changes that occur at plant surfaces under such conditions could not be probed under realistic environments. Using atomic force microscopy (AFM) we are studying cuticular surface structural changes under various environmental conditions to examine how processes such as lipid abrasion and erosion, degree of hydration, thermal fluctuations and mechanical damage influence cuticular structure and surface flexibility on the nanometer scale.

9702974 Moisture Transport in Paper Materials Under Dynamic Conditions
Chatterjee, S.G. **Grant 97-35504-4795**

SUNY College of Environmental Science & Forestry **New Investigator/Strengthening Award**
Faculty of Paper Science and Engineering **$60,000**
Syracuse, NY 13210 **2 Years**

The moisture content of a paper sheet or board is a key parameter which affects its mechanical and electrical properties. There is a severe loss in the strength properties of paper with increasing moisture content which is accentuated under cyclic humidity conditions. We propose detailed experimental and theoretical investigations in (1) moisture sorption equilibria with special attention to the interior of the hysteresis region, (2) transport mechanisms of moisture through paper webs, and (3) the uptake and release of moisture under ramp and cyclic changes of the relative humidity (RH) of the external environment. In order to understand and quantify moisture changes occurring in a paper board under a changing external RH, all of the above three areas are linked to one another and have to be studied systematically.

The outcome of the research will be a coherent body of knowledge about the hysteresis observed in the equilibrium moisture content under equilibrium RH conditions and the mechanisms of moisture transport in paper under dynamic RH conditions. This will enable paper physicists to relate the effects of changing RH to the warp and dimensional stability of paperboard cartons and lead to better design of packaging materials. The research proposed here will be useful in developing consistent pre-conditioning procedures for paper samples in paper testing laboratories and will also be applicable to the drying of wood and paper, thus leading to their better utilization.

9703349 Assembly of the Iron-Protein of Nitrogenase (Is the NifM protein peptidyl-prolyl *cis/trans* isomerase?)
Gavini, N. **Grant 97-35305-4741**

Bowling Green State University **Strengthening Award**
Department of Biological Sciences **$90,000**
Bowling Green, OH 43403-0020 **2 Years**

The air is composed of 79% nitrogen gas (N_2), however, N_2 must be converted to a fixed form before it can be used to synthesize proteins, nucleic acids and other cellular components. Therefore, nitrogen fixation is of fundamental importance in the biosphere. The N_2-fixing bacteria have an enzyme called nitrogenase encoded by *nifHDK* genes. Besides these structural genes that encode nitrogenase, there are a number of *nif*-specific genes and their protein products. Although the functions of many of these genes have not been determined, the genes have been shown to be necessary for the maturation, assembly and reactivity of nitrogenase. We compared the *nifM* genes and generated a consensus sequence which was then compared to the conceptually translated nucleotide sequence data bases. This comparison showed that the carboxyl terminal region of the NifM-proteins shares significant homology with the family of proteins called peptidyl-prolyl *cis/trans* isomerases. As a first step to identify the

functional properties of the *nifM* product, we propose to purify the NifM-protein and to test its ability to f unction as a peptidyl-prolyl *cis/trans* isomerase. Since the levels of the *nifM g*ene expressed from its native promoters are very low, we need to construct a strain that can overexpress the NifM-protein. The specific goals of the research in my laboratory during this grant period are as following: 1. To construct strains that can overexpress functional NifM protein, 2. To purify the NifM protein to homogeneity, 3. To test its ability to function as a peptidyl-prolyl *cis/trans* isomerase.

9703943 Effects of Tillage Regime and Predator Interaction on Biological Control
Hodge, M.A. **Grant 97-35311-5116**

The College of Wooster **Seed Grant**
Department of Biology **$49,214**
Wooster, OH 44691-2363 **2 Years**

Several studies have shown that combinations of different species of insect predators may be very effective at controlling agricultural pests. However, different species of predators may compete with or prey on each other, reducing the potential for effective biological control. Competition, cannibalism and predation are interactions that are especially relevant for generalized predators such as spiders and carabid beetles, which overlap in size, activity, habitat and feeding habits. This proposal concerns such interactions among these two predominant ground-dwelling predators in soybean fields maintained under conventional tillage versus those maintained under conservation tillage. Several studies have shown that conservation tillage regime, which leaves weedy debris on the ground, enhances populations of both beetles and spiders. This study will examine whether the potential advantage of more predators is offset by negative interactions between them. I will characterize the beetle and wolf spider fauna in conventional tillage and conservation tillage soybean fields, and examine the nature of interactions between overlapping predator species (spider-spider; beetle-spider; beetle-beetle) in laboratory trials. Based on these laboratory studies I will examine interactions between specific combinations of species and their impact on pest populations in the field using experimental field enclosures. Ultimately, I will measure how the interaction between predator species combined with tillage regime influence soybean productivity. The information obtained on predator ecology will have implications for habitat management practices and pesticide application, all of which are important in assessing the trade-offs between biological control and other pest management strategies.

9701228 Signal Transduction Pathways Controlling Plant Growth Adaptations to Water Deficit
Conley, T.R. **Grant 97-35100-4227**

Oklahoma City University **New Investigator/Strengthening Award**
Department of Biology **$110,700**
Oklahoma City, OK 73106-1493 **2 Years**

When a corn seedling lacks sufficient water for normal growth, elongation of the shoot decreases or stops altogether. In contrast, the root system of the seedling continues to grow, presumably as a means of finding water and bringing it to the plant. The regulatory mechanism that controls plant growth adjustments to water stress is unknown. In responding to other environmental cues, such as light and temperature stress, plants utilize signaling pathways that are similar to those used by yeast and animals. It is likely that plants use similar processes to control their responses to water stress One important class of molecules that participates in virtually all signaling pathways is that of the protein kinases. The focus of this project is the isolation of a protein kinase that is rapidly activated by water stress in the roots of corn seedlings. This protein kinase is found in the roots before the onset of water stress and is activated in the region of the root where growth occurs. Preliminary work has shown that this molecule may function as a switch at an early step in controlling the growth adjustments of water-stressed corn seedlings. Isolating this protein may be an important step towards understanding how plants control their responses to drought and may facilitate progress towards genetic manipulation of plants with improved drought tolerance.

9703704 Enhanced Capacity for Assessing Micronutrient Interactions and Immunity
Arquitt, A.; Stoecker, B.J. **Grant 97-35207-4774**

Oklahoma State University **Equipment Grant**
Department of Nutritional Sciences **$32,500**
Stillwater, OK 74078-6141 **1 Year**

The Cobas Helios 5Diff hematology instrument allows the evaluation of the effects of micronutrients and their interactions on blood cell populations. The instrument is suitable for use in both human and animal studies; in addition to the species preprogrammed, the operator can independently adjust any of the 13 different thresholds so that analyses for additional species can be programmed. This instrument requires small sample sizes; as little as 25 uL of blood will provide the usual hematological parameters - hemoglobin, hematocrit, mean corpuscular hemoglobin, mean corpuscular hemoglobin concentration, mean platelet volume, and counts of both red and white blood cells and platelets. Using 125 uL additional whole blood provides complete 5

part differential analysis of white blood cells. These cells are important in the differentiation of immune system responses to antigens. The small sample volume required makes these analyses realistic in small animal models of human diseases. Studies currently underway that will use this instrument include trace element supplementation in humans at risk of cardiovascular disease, effects of endotoxin on trace element absorption and retention in weanling pigs, effects of isoflavones on bone and immune function, and trace element effects in a diabetic animal model. Thus, with this instrument the Department of Nutritional Sciences will be able to provide a more complete description of the effects of micronutrients, including interactions between them, on blood cells and the immune system in human and animal studies.

9704005 Automated Microbial Fermentation System for Enhancing Bovine Research
Confer, A.W.; Clinkenbeard, K.D. **Grant 97-35208-4718**

Oklahoma State University **Equipment Grant**
Department of Anatomy, Pathology and Pharmacology **$43,174**
Stillwater, OK 74078-2007 **1 Year**

Scientists at Oklahoma State University are actively studying bovine shipping fever pneumonia, the major cause of disease and economic loses to the beef cattle industry of North America. This disease is associated with bacterial infections, especially with *Pasteurella haemolytica* and *Pasteurella multocida*. Study of this disease requires growth of these bacteria under strict culture conditions to determine bacterial proteins that are important for causing disease or for stimulating immunity to the disease. These proteins include toxins, bacterial surface proteins, and proteins expressed only when bacteria are grown in conditions of low iron availability. Once the important proteins are determined, large quantities of the bacteria must be grown so that enough of the desired proteins can be purified to determine their potential as a vaccine. Use of a 1 0-liter fermentor system purchased through the USDA NRI Competitive Grants Program will facilitate shipping fever research by allowing scientists to grow large quantities of the bacteria under the growth conditions required by the bacteria to produce the specific protein at maximum quantities. Use of this fermentor system will further our knowledge of shipping fever and assist in developing effective vaccines.

9704009 Flow Cytometry System for Enhancement of Bovine Disease Research
Wyckoff, J.H. III **Grant 97-35208-4720**

Oklahoma State University **Equipment Grant**
College of Veterinary Medicine **$50,000**
Stillwater, OK 74078-2006 **1 Year**

This award will be used to partially fund the acquisition of a flow cytometer. This instrument will provide capability to assess surface molecules of Iymphocytes, pathogens and cells of the uterus as well as sort separately different populations of bovine cells or bacterial cells. All proposed users perform research on cattle or bovine pathogens. Specific diseases and research programs include immunity and vaccine development of Bang's disease (also called brucellosis, caused by *Brucella abortus*) and bovine tuberculosis (caused by *Mycobacterium bovis*) shipping fever pneumonia (major causative agent is *Pasteurella haemolytica*) gall disease (also known as anaplasmosis, (caused by *Anaplasma marginale*) and establishment and maintenance of pregnancy in cattle. More specifically, the instrument will enable us to evaluate more precisely various T Iymphocyte populations, cells thought to be necessary for immunity, in brucellosis, tuberculosis and shipping fever. The physical characteristics of molecules from pathogens considered to be important vaccine targets will be evaluated in shipping fever and anaplasmosis. Molecular mechanisms involving leukotoxin, a major molecule involved in the pathogenesis of shipping fever pneumonia, will be further evaluated using this instrument. Steriod hormone receptor expression in the bovine uterus will be assessed in research investigating the role of the estrogen receptor presence/absence in the pregnancy. All these research programs will be greatly enhanced by the acquisition of this instrument and application of this technology.

9701847 Incentives for Health Claim Research
Childs, N.M.; Pan, J. **Grant 97-35400-4528**

St. Joseph's University **Strengthening Award**
Food Marketing, Mathematics **$110,000**
Philadelphia, PA 19131 **2 Years**

The Nutrition Labeling and Education Act (NLEA) permitted the use of approved health claims on the food label, which was designed to fulfill the FDA's new education mandate under the NLEA, and to encourage consumers to choose healthier foods. Under the existing NLEA format, all health claims are generically worded and available to all products whose nutrition profiles qualify for the use of claims, regardless of who invested in the research. This "publicness" of the health claims has not spurred a major investment in private sector nutrition research.

Using both empirical market analysis and market share models, we will document the usage of health claims in food industry, study the competitive strategies of companies in the current market environment, compare the behaviors of market dominant food

cooperatives and individual non-dominant food processors, and provide further explanation to the current low level of health claim activities.

Interpolating the data from empirical market analysis, quantitative equilibrium models will be constructed to assess incentive options such as market exclusivity, licensing and tax incentives. Computer simulation will be performed for the equilibrium outcomes on some of these options under various market situations. Our objective is to develop appropriate incentive policies for nutrition research.

9703737 Cell Wall Composition and Metabolism in Non-Articulated Laticifers
Serpe, M.D. **Grant 97-35311-5157**

Cayey University College **Seed Grant**
Department of Biology **$32,255**
Cayey, PR 00736-0000 **2 Years**

Non-articulated laticifers are long cells that contain latex, a conspicuous and often white fluid that oozes from some plants upon injury. These laticifers show unusual growth characteristics. They elongate indefinitely without cell division, thus becoming giant cells that extent throughout the whole plant. Little is known about the mechanisms that determine the growth of these cells. My interest is to investigate such mechanisms in non-articulated laticifers from *Euphorbia heterophylla*, a species closely related to poinsettias. Plant cells, including non-articulated laticifers, are surrounded by a cell wall, a rather rigid structure whose composition and metabolism ultimately determines plant cell growth. To gain an insight into the growth mechanisms of non-articulated laticifers, I will separate laticifer segments from other cell types and determine the carbohydrate composition of laticifer walls. Also, I will attempt to identify enzymes that can cause changes in the carbohydrate component of laticifer walls. Knowledge in these areas may provide valuable clues about the mechanism of laticifer elongation. Furthermore, because of the uncommon growth characteristics of these cells, this research may reveal processes of growth regulation that are unique among plant cells.

9703550 A Physical Dairy Cow Model for Evaluating Sprinkle and Fan Cooling Systems
Perez-Munoz, F.; Santana, C.S.; Randal, P.F. **Grant 97-35208-4777**

University of Puerto Rico, Mayaguez **Seed Grant**
Agricultural Engineering Department **$50,000**
Mayaguez, PR 00681-5000 **2 Years**

Milk production and conception rates of dairy cattle suffer under heat stress. Evaporative cooling systems such as sprinkle and fan systems have been shown to be practical ways to significantly reduce dairy cattle's heat stress and, thus, increase productivity. Sprinkle and fan systems, however, have not been fully optimized. Work is needed to determine efficient water application and ventilation rates that will minimize the amount of wasted water and energy while maintaining appropriate cooling. This effort seeks to develop a physical model of a dairy cow that could be used to collect data leading to the optimization of sprinkle and fan systems.

Successful use of physical models to study animal-environment heat transfer characteristics is reported in literature. The model proposed in this study will be of actual cow size and made of metal pipes. Heating units and thermocouples installed in the model will simulate internal heat generation and monitor temperature, respectively. Measurement and control will be achieved through a personal computer equipped with a data acquisition and control system. Model validation will be done by comparing the model's temperature data with data from real cows under the same sprinkle and fan system conditions. The model could provide a unique tool to do many heat loss related studies, including sprinkler and fan cooling, radiation heat exchange, and effects of air velocity.

9703719 Mercury Porosimetry for Soil Ecological and Natural Resources Research
Amador, J.A.; Görres, J.H. **Grant 97-35106-5059**

University of Rhode Island **Equipment Grant**
Department of Natural Resources Science **$25,000**
Kingston, RI 02881-0804 **1 Year**

More than half of the volume of soils is constituted by voids. These voids, or pores, vary in size from a few nanometers to millimeters in diameter. The distribution of pore sizes determines the ability of soil to hold and transmit water and gases, to support the growth and activities of plants, soil fauna and microflora, and to interact with pesticides. We will study the pore structure of soils as it relates to the ecology of nutrient cycling by soil microflora and fauna and to the persistence of pesticides in soil using a mercury intrusion porosimeter. This instrument measures the pressure required for intrusion or extrusion of a volume of mercury in a porous medium and relates it to pore diameter. The pore size distributions obtained will be used to construct and test a model in which the ecological interactions among soil organisms in agricultural soils

are constrained by their body size and the diameter of soil pores. We will also evaluate agricultural practices that can lead to entrapment or release of pesticides in very small pores within soil particles (nanopores) and which may control their persistence in soil.

The use of high-yield, mechanical pulps can improve fiber use efficiency, particularly when blended with chemical pulps to enhance sheet structure, a determinant of paper quality. We will probe paper structure with mercury porosimetry to verify a sheet structure model that can be used to identify favorable pulp blends.

9703935 Forest Ecosystem Carbon, Nitrogen and Phosphorus Retention Processes after Agricultural Abandonment
Compton, J.E. **Grant 97-35106-4803**

University of Rhode Island **Seed Grant**
Department of Natural Resources Science **$49,805**
Kingston, RI 02881-0804 **2 Years**

The landscape of New England is a complex mosaic of forests recovering from historical agricultural use, more recent forest management, and encroaching urbanization. The history of these forests could play an important role in their response to disturbance and to widespread change such as increased atmospheric N deposition. Previous work in central Massachusetts indicated that site C and P storage, soil C:N ratios, and rates of nitrogen cycling were strongly impacted by land-use history. I propose to examine the recovery of processes resulting in the storage of carbon, nitrogen and phosphorus in the forests of western Rhode Island. Agricultural land-use history and forest management will be mapped within the W. Alton Jones campus of the University of Rhode Island and combined with existing geographic databases on soils, present vegetation and geology. The rate of carbon, nitrogen and phosphorus storage will be measured in regrowing forests on abandoned agricultural sites, by sampling soils and vegetation across a time sequence of sites with different abandonment dates. My long-term goal is to develop a base of information on forest C, N and P cycling in order to determine the impact of present-day forest management on growth and nutrient cycling, and to ultimately link this information to study the composition of surface waters and nutrient loading in coastal watersheds.

9703460 Molecular Imager to Enhance Life Science Research Program at URI
Fischl, A.S.; Bradley, T.M. **Grant 9735208-4723**

University of Rhode Island **Equipment Grant**
Department of Food Science and Nutrition **$35,025**
West Kingston, RI 02892 **1 Year**

This equipment grant is for a Molecular Dynamics Storm 840 imaging system, a multi-purpose phosphor and fluorescence imaging scanner that is used for the detection and quantification of radio labeled and fluorescent biomolecules from electrophoresis gels, membranes and TLC plates. Our Life Science research laboratories at the University of Rhode Island routinely perform a wide variety of techniques for the detection and analysis of nucleic acids, proteins and lipids using a number of different labeling and detection methods. Many of these methods suffer from their inability to rapidly detect and accurately quantify images from which meaningful data can be obtained. The Storm imaging System will provide our investigators with sensitive detection and quantification capabilities that are currently not available at the University of Rhode Island. The Storm unit will support projects investigating the metabolism and function of membrane lipids in yeast, the role of heat shock proteins in conferring protection against osmotic shock upon transfer of salmon to seawater, and genetic mechanisms of disease resistance and pesticide resistance in silkworm. The availability of a Molecular Dynamics Storm imaging system represents a significant addition to our research infrastructure and enhances our graduate research program and competitiveness in biochemistry, molecular biology and aquaculture related research activities.

9702704 Mucus-inducible Genes and Proteins of *Vibrio anguillarum* as Vaccine Candidates
Nelson, D.R. **Grant 97-35204-4811**

University of Rhode Island **Strengthening Award**
Department of Biochemistry, Microbiology, and Molecular Genetics **$100,000**
Kingston, RI 02881-0800 **2 Years**

It has been shown that the fish gastrointestinal tract is a major portal of entry for the bacterium *Vibrio anguillarum*, the causative agent of vibriosis. Vibriosis is one of the most destructive bacterial diseases of fish. It causes significant losses to the aquaculture industry and can limit the production of finfish in seawater. Though normally considered an infection of marine fish, *V. anguillarum* can become established in fresh water with devastating results to freshwater fish. We have demonstrated that when this bacterium is grown in salmon intestinal mucus, new outer membrane proteins are produced. We hypothesize that these new mucus-inducible outer membrane proteins are necessary for growth in gastrointestinal mucus and may serve as vaccine candidates for the development of improved vaccines against vibriosis. We propose to: 1) clone and characterize one of the genes that encode

a mucus-inducible protein (MIP) of *V. anguillarum*, 2) determine the function of the cloned MIP during growth in mucus; and 3) determine whether a mutant strain of *V. anguillarum* no longer able to make the MIP is avirulent, whether such a mutant may serve as a live vaccine strain, and whether the purified MIP may serve as a vaccine candidate. Information gained as a result of this investigation should enable the development of improved and more efficacious vaccines against vibriosis, as well as provide new methods for the development of vaccines against other potential fish pathogens. The development of improved vaccines will enhance the growth and economic success of the aquaculture industry.

9701965 Gordon Research Conference on "Photosynthesis: Biophysical Aspects''
Okamura, M.Y. **Grant 97-35306-4398**

Gordon Research Conference **Strengthening Award**
c/o University of Rhode Island **$8,000**
West Kingston, RI 02892-0984 **1 Year**

The goal of photosynthesis research is to answer the question of how sunlight is converted into chemical energy in living systems. Current research has been focussed on structure and function of the molecular complexes that compose the photosynthetic machinery located in cell membranes of plants and photosyntheric bacteria. Major advances have been made in recent years with biophysical approaches to photosynthesis. The Gordon Conference on "Photosynthesis:Biophysical Aspects" brings together leading researchers from diverse fields; structural biology, biophysics. spectroscopy, molecular biology, synthetc chemistry, and computational biophysics to exchange ideas and report recent fndings. Some of the research to be reported include the following: molecular structures of protein complexes determined using x ray diffraction and spectroscopic techniques, the temporal sequence of events resolved using pulsed laser experiments, the simulation of molecular models for energy conversion processes using new computational methods. The results of this conference will advance our understanding of photosynthesis which forms the basis for crop productivity.

9703648 Dietary Manipulation of Metabolism in Salmon Smolts
Tremblay, G.C. **Grant 97-35206-5288**

University of Rhode Island **Strengthening Award**
Department of Biochemistry, Microbiology and Molecular Genetics **$120,000**
Kingston, Rl 02881-0000 **2 Years**

Juvenile salmon must undergo major metabolic changes before they are able to migrate from the freshwater streams, where they were hatched, to the open ocean, where they grow to maturity. This salt-water challenge is gradual in nature, but it is quite abrupt in commercial aquaculture, where salmon are transferred directly from freshwater hatcheries to sea water netpens. Salt-water tolerance requires considerable expenditure of energy, yet transfer occurs at a time in the life cycle of salmon when carbohydrate-energy reserves in the liver are virtually depleted. Losses upon transfer to sea water can be high. There are specific nutrients known to stimulate deposition of carbohydrate-energy reserves in the liver, and we propose to feed such nutrients to juvenile Atlantic salmon for several months prior to sea water transfer. We plan to determine whether feeding these dietary additives prevents depletion of carbohydrate-energy reserves in the liver, and whether such action is associated with biochemical evidence of improved salt water tolerance. We will also determine whether salmon fed such diets exhibit greater sea water survival and growth.

9703459 Request for a Fermenter System
Traxler, R.W. **Grant 97-35501-4637**

University of Rhode Island **Equipment Grant**
Department of Food Science and Nutrition **$ 25,612**
West Kingston, RI 02892-1802 **1 Year**

This project provides a 15 Liter Bio-Reactor (Fermenter) package which includes an ADI BioController for precise control of those factors which affect the biological activity of bacteria, yeast and other microorganisms. Those control features include pH, dissolved oxygen and other gas concentrations, agitation speed, and temperature using computer driven BioSpert software which monitors these parameters and can be programed to change a parameter upon command. These changes influence the biological capability of the organisms (biomass) which is important to the teaching and research infrastructure of the university which uses the biomass for emerging interests in agricultural, food, marine and environmental biotechnologies. The addition of this equipment to our research infrastructure will enhance Life Science graduate research and senior undergraduate research experience opportunities. Current projects which will be supported by this instrumentation are (1) Studies on oxygen limitation and ethanol stresses in yeast, (2) Stereospecific bioconversion of aromatic compounds in which the stereo prefix (i.e., cis or trans)

is related to the biological activity of the product, and (3) Biosynthesis and function of lipids in yeast membranes which control fundamental activities of yeast. The overall effect of this project will be to increase our research productivity and competitiveness.

9703772 High Yield Sustainable Aquaculture
Brune, D.E.; Eversole, A.G.; Hammig, M.D.; Schwedler, T.E.; Collier, I.A. **Grant 97-35209-5127**

Clemson University **Strengthening Award**
Department of Agricultural and Biological Engineering **$115,000**
Clemson, SC 29634-0357 **2 Years**

Aquaculture is increasing at an annual rate of 20% and has become a one billion dollar industry in the U.S. providing nearly 15% of our seafood. Due to limited water supplies, future aquaculture development will likely require captive water systems, where the culture water is treated and reused. Researchers at Clemson University have demonstrated that current industry pond fish production of 5,000 lb/acre can be increased to 12,000 lb/acre through the use of an innovative new technique, The Partitioned Aquaculture System (PAS). This system couples high density raceway culture of fish with paddle wheel-driven high rate algal growth basins for treatment of wastes allowing 100% reuse of culture water in 2-4 acre self-contained culture units. This high productivity from small modular units is ideally suited for small or medium sized farmers. Research to date, suggests that an additional doubling of production to over 20,000 lb/acre may be possible by coupling the fish/algal system to co-culture of filter-feeding, organisms such as tilapia (*Oreochromus niloticus*) and freshwater bivalves (e.g.*Elliptio sp.*). This technique would provide a method to quadruple current pond aquaculture production while recovering wasted nitrogen and phosphorus discharges, which currently pose a eutrophication or pollutant threat to surface and groundwater supplies. This 2-year study seeks to prove this concept of controlled catfish/algal/herbivore co-culture, resulting in a system with 100% captive water, while recovering 50-75% of input nutrients. The overall goal of this research will be to evaluate the PAS concept as a high yield sustainable aquaculture practice that may have widespread application in the U. S.

9702671 Involvement of Plant Inducible Bacterial Promoters/Genes in Root Colonization
Kluepfel, D.A. **Grant 97-35303-5105**

Clemson University **Strengthening Award**
Department of Plant Pathology and Physiology **$62,462**
Clemson, SC 29634-0377 **2 Years**

The term, rhizosphere, defines the zone surrounding plant roots that is influenced by the root and its exudates. This environment is complex biochemically and is a region of intense microbial activity. However, root exudate composition is continuously changing as a function of environment, plant age, and developmental stage. These changes modulate bacterial gene expression, influencing such behavior as colonization, competition and stress response. Here we propose a series of experiments designed to examine the interaction between plant roots and members of the bacterial genus Pseudomonas. Using a promotorless xylE reporter gene we have identified four Pseudomonas Tn5::xylE mutants that are induced when grown in the rhizosphere. An important discovery was that the ability of root exudates to modulate xylE expression in these mutants was plant species dependent. We propose to characterize both the temporal and plant species dependent nature of each of these root-exudate modulated bacterial promoters/genes. This will be followed by an examination of the role these tagged genes play in root colonization and competition. The utilitarian use of rhizosphere-inhabiting microorganisms in biological control, plant growth promotion, and bioremediation are goals pursued by many microbiologists. A complicating issue which plagues this approach is our lack of understanding of both the ecological parameters that regulate bacterial gene expression in the rhizosphere and the genes/promoters being regulated. The results from the research proposed here will move us closer to wide spread predictable use of microbial biological control agents in sustainable agricultural.

9703477 Aquaculture of Amphioxus (Lancelets)
Ruppert, E.E.; Frick, J.E. **Grant 97-35208-4703**

Clemson University **Seed Grant**
Department of Biological Sciences **$49,921**
Clemson, SC 29634-1903 **2 Years**

The long-term goal of the project is to aquaculture lancelets, a novel and unexploited source of animal protein, for human consumption or as animal feed. The immediate goals are to determine the effects of various foods and environmental factors on the growth and reproduction of lancelets. Lancelets are small (4-5 inches) fishlike animals that resemble minnows or anchovies. They burrow in marine sand, like sand eels, and feed on plankton, similar to clams and oysters. Although they resemble fishes in body form, they lack a skull, vertebrae, bones, and scales and are classified apart from the fishes and other vertebrate animals on the basis of those absences. Lancelets replace bone and cartilage with muscle and are thus among the meatiest of all animals. Being virtually all muscle, they are ideal candidates for use as a high-quality protein (meat) source for human or farm-animal

consumption. Lancelets are widespread along the coast of southeastern United States and elsewhere in warm seas. Their natural populations can exceed a thousand individuals per square yard of sand. Such populations, though vast, are not harvested as food in the United States and no one has yet attempted to aquaculture the animals. In parts of China and Taiwan, however, lancelets have been consumed by humans for centuries and the current fishery, located in a small bay, yields between 35 and 200 tons of lancelets annually. Lancelets have an enormous potential in aquaculture as an easily maintained, disease-resistant source of high-quality protein.

9703490 Development of a Clinical Indicator of Ammonia Toxicosis in Channel Catfish
Tomasso, J.R. **Grant 97-35208-4684**

Clemson University **Seed Grant**
Department of Aquaculture, Fisheries and Wildlife **$49,949**
Clemson, SC 99634-0362 **2 Years**

Over 400 million pounds of farm-raised channel catfish are marketed in the United States each year. Almost all of these fish are grown in earthen ponds. During the culture process, the concentration of ammonia in the pond water may increase due to the metabolism by the fish of protein present in the fish feed. Ammonia will decrease growth rates in fish resulting in less than optimal farm production. Presently, there is no method to quantitatively predict the impact of environmental ammonia on growth of channel catfish in ponds.

This project will seek to identify one or more physiological indicators of ammonia toxicosis in channel catfish that correlate with reduced growth. Fish will be exposed to environmental ammonia in the laboratory for up to eight weeks, weighed and analyzed. Brain monoamine (such as adrenalin) concentrations and liver enzyme activities will be evaluated as potential indicators. In previous studies, brain monoamine concentrations and liver enzyme activities have been shown to change in ammonia-exposed fishes.

If a physiological indicator that correlates with reduced growth is found, a study will be designed to see if the correlation is present in fish reared in ponds. If the correlation persists under pond conditions, the physiological indicator may provide a useful management tool on catfish farms by providing an estimate of the impact of ammonia on fish growth.

9701358 Biochemical and Biophysical Characterization of *Arabidopsis* MADS Domain Proteins
Krizek, B.A. **Grant 97-35304-4690**

University of South Carolina, Columbia **New Investigator Award/Strengthening Award**
Department of Biological Sciences **$90,000**
Columbia, SC 29208-001 **2 Years**

Molecular genetic studies in the model plant *Arabidopsis thaliana* have identified a family of genes that play important roles in flower development. Two members of this MADS box family, *APETALA3* (*AP3*) and *PISTILLATA* (*PI*), are required for the development of petals and stamen in a flower. AP3 and PI form a heterodimer that binds to DNA and is thought to act as a transcription factor, regulating the expression of a set of genes required for organ development. Although AP3 and PI form homodimers, *in vitro* data indicates that the homodimers do not bind DNA. To understand the basis for this DNA-binding specificity, biochemical and biophysical characterization of the proteins is necessary. We will develop an expression system for AP3 and PI so that these methods will be possible in the future. Molecular modeling of the AP3/PI heterodimer, based upon the known structure of another MADS domain protein, will be performed in order to identify amino acids that may be responsible for the ability of the heterodimer but not the homodimers to bind DNA. The role of these amino acids will be investigated by making mutations at these positions and assaying the resulting sequence variants in *in vitro* DNA-binding studies and in vivo for their ability to rescue the respective (*ap3* or *pi*) mutant. Characterization of the interactions between MADS domain proteins that result in DNA binding dimers is a first step towards understanding the regulatory roles of MADS domain proteins in plant development.

9703708 Glycanic Structure Recognized by *Escherichia coli* K88ab lectin
Grange, Ph.A. **Grant 97-35208-4704**

South Dakota State University **Seed Grant**
Veterinary Science Department **$50,000**
Brookings, SD 57007-1396 **2 Years**

Enterotoxigenic *Escherichia coli* are bacteria which are a major cause of disease in swine. In the small intestine of pigs, there are receptors which permit specific types of bacteria to bind to the wall of the intestine. Some pigs do not have receptors for certain bacteria, and thus are resistant to disease caused by that bacteria. We are studying the structure of the receptors expressed by pigs that are susceptible to enterotoxigenic *Escherichia coli* infections, and the complementary molecules produced by disease-resistant pigs. We have identified a receptor recognized by some strains of enterotoxigenic *Escherichia coli*. This receptor is a

glycoprotein. We propose to use this glycoprotein as a model to determine the structure of the receptor necessary for enterotoxigenic *Escherichia coli*, to bind to the small intestine. Determination of the structure of the receptor will provide us a more complete understanding of the molecules involved in recognition by bacteria, and will enable us to design drugs that block the binding of enterotoxigenic *Escherichia coli* to the small intestine, thus, preventing disease.

9702751 Virological, Immunological, and Molecular Components of Reproductive PRRS
Rowland, R.R.R.; Benfield, D.A., Cafruny, W. **Grant 97-35204-5071**

South Dakota State University **Strengthening Award**
Department of Biology/Microbiology **$158,955**
Brookings, SD 57007 **3 Years**

Porcine reproductive and respiratory syndrome (PRRS) has emerged as the most economically important disease of swine in the 1990's. The infection of pregnant gilts and sows with PRRS virus (PRRSV) produces a spectrum of reproductive disease outcomes, ranging from fetal death and abortion to persistent infection of piglets. Even though abortion and stillbirths are the most noticeable effects, the impact of persistent infection is beginning to be realized. Ongoing work on persistent PRRSV following intrauterine infection suggests that PRRSV causes problems in the nursery and persists for several months and is eventually re-introduced into the next breeding cycle. The anatomy, reproductive physiology, and immunology of the pig provide an ideal model for understanding how PRRSV causes reproductive disease. The overall goal of this project is to monitor changes in virus replication and immune cell cytokines at the maternal-fetal interface during the infection of pregnant pigs. This requires the use of a variety of techniques including virus isolation, polymerase chain reaction, in situ hybridization, immunohistochemistry and enzyme-linked immunoassay (ELISA). The first objective is to develop a disease model by comparing three strains of PRRSV that represent the whole range of PRRSV virulence. The second objective is to determine if persistently-infected female pigs pass PRRSV vertically to developing fetuses.

9703938 Significance of Different Sources of Organic Sulfur to Forest Surface Soils
Spratt, Jr., H.G. **Grant 97-35106-5063**

University of Tennessee, Chattanooga **Seed Grant**
Department of Biological and Environmental Sciences **$49,969**
Chattanooga, TN 37403-2598 **2 Years**

The leaching of nutrient cations (e.g. K^+, Ca^{2+}, and Mg^{2+}) from forest soils as a result of acidic deposition has been described for a number of different forest ecosystems. Retention of sulfate, within forest ecosystems, as organic S, has been found to reduce leaching of nutrient cations from forest soils. As a result of this relationship between organic S and nutrient cations, factors that contribute either to reduced rates of organic S production or enhanced rates of organic S decomposition may result in the loss of nutrient cations from the ecosystem. In a forest ecosystem organic S can be formed in two principle ways: assimilation by plants or by microorganisms. Plant-derived organic S is composed of carbon bonded S (C-S), while microbial-derived organic S can contain both carbon bonded S and ester sulfates (C-O-S). Decomposition rates of these different types of organic S are known to differ. Therefore, the origin of forest soil organic S may play a role in the potential for loss of nutrient cations by leaching if the sources of organic S vary in their inherent degradability. This may be especially important in forests from which timber is harvested, with organic S production shifting primarily from plant- to microorganismal-based. The major emphasis of this proposed work is to determine the sources of organic S in Missouri Ozark forest surface soils, and the relative importance of organic S, having different sources, to nutrient cation retention in these soils.

9703426 Physiological and Genetic Analysis of Maize Responses to Ultraviolet Radiation
Stapleton, A.E. **Grant 97-35106-5062**

University of Tennessee, Chattanooga **Seed Grant**
Department of Biological and Environmental Sciences **$50,000**
Chattanooga, TN 37403 **2 Years**

Plants are essential to our lives; they produce the oxygen that we breathe, the food we eat, and the clothes that we wear. The ability of plants to grow in our changing environment depends on the ability of those plants to adapt to environmental factors such as increased ultraviolet radiation. Plants perceive UV radiation and can attenuate and repair UV-induced damage. Genetic analysis of plant responses to UV radiation provides a powerful method to dissect the mechanism of these UV responses. We have used a morphological response, UV-induced leaf rolling, to isolate maize mutants that have altered responses to ultraviolet radiation (*leaf response to ultraviolet* or *lru* mutants). The mutants were generated by insertion of a transposon (a jumping gene) into the maize genome. The first step in "cloning a mutant gene" isolated from a transposon mutagenesis is identification of a DNA fragment that specifically reacts with the inserted transposon and is found in only *lru* mutant plants; closely related plants that are not UV-sensitive are used for comparison. We will identify such a cosegregating fragment, clone it so that it is available

in sufficient quantity for further analysis, and analyze the cloned gene in complete detail (by DNA sequencing). Molecular characterization of *lru* genes that can be mutated to UV-sensitivity is essential for manipulation of plant genomes for crop improvement and for better understanding of the diversity of responses to ultraviolet radiation in all living organisms.

9703441 Biochemical and Molecular Characterization of Two Flavanone Branch Point Enzymes
McIntosh, C.A. **Grant 97-35311-5110**

East Tennessee State University **Equipment Grant**
Department of Biological Sciences **$12,897**
Johnson City, TN 37614-0703 **1 Year**

Flavonoids are a group of chemicals made by plants that are important for flower color, fruit color, some fruit flavors, and protecting leaves from ultra-violet light damage. Some flavonoids can cause insects to avoid eating plants, and some flavonoids play important roles in attracting insect pollinators. Because they are present in larger amounts and since plants are such a large part of the human diet, there has been a lot of research investigating the effects of flavonoids on human physiology. For example, some of the compounds have anti-inflammatory properties and others can prevent tumor formation. This research is designed to characterize two specific enzymes in an early branch point of the flavonoid biosynthetic pathway and eventually elucidate the biochemical, physiological, and molecular control of this branch point. the research will advance our understanding of how much and what specific kinds of flavonoids different plants make. Once understood, it may be possible to develop plant varieties with altered flavonoid-producing abilities. Liquid scintillation counting (LSC) is a critical and integral component of the enzyme assay technology used in this research. The two branch point enzymes are highly specific as to the flavonoid substrate required and position of attachment of side groups. Radio-label tagging of substrates and monitoring of label appearance in products affords both rapid and sensitive measurement of enzyme activity. This proposal is a request for 50% of the funds necessary to purchase a LSC system to be housed in my laboratory in the Department of Biological Sciences.

9703727 Incubator Shaker for RFLP Mapping in Soybean
Gresshoff, P.M. **Grant 97-35311-5111**

University of Tennessee **Equipment Grant**
Institute of Agriculture **$5,094**
Knoxville, TN 37996-4500 **1 Year**

Legumes form root-outgrowths (nodules), in which nitrogen fixation for the fertilizer use of the plant is possible. Plants, like soybean, possess genes that control the formation of nodules and their number. We isolated a soybean super-nodulation mutant in which the internal regulation of nodule number is diminished. We found a molecular marker close to this gene *(nts-1)* and are using it to isolate the entire DNA region using bacterial artificial chromosomes. The project involves growth of many bacterial clones, from which DNA will be isolated. This bacterial growth requires a controlled environment incubator shaker, for both large scale and small scale preparation. Through discovering the nature of the *nts-l* gene, or at least the region in which it resides, we hope to better predict the anticipated performance of soybean varieties and possibly lessen the N-fertilizer requirements for agriculture.

9703688 PCR Thermocycler: Diagnosis of Active Equine Herpesvirus 2 Infection
Lindquester, G.J. **Grant 97-35208-4776**

Rhodes College **Equipment Grant**
Department of Biology **$7,846**
Memphis, TN 38112-1624 **1 Year**

The proposal is for the purchase of a polymerase chain reaction (PCR) thermocycler and accessories. The project of the principle investigator involves the development of a reverse transcriptase PCR (RT-PCR) assay for the detection of active equine herpesvirus 2 (EHV2) infection in horses and its use in correlating active infection and disease for this agent of unknown etiology. EHV2 has been isolated from up to 90% of apparently healthy horses and has been implicated in immunosuppression in foals, upper respiratory tract disease, conjunctivitis, general malaise, and poor performance. As a gammaherpesvirus latent in B lymphocytes, it is hypothesized that EHV2 is a significant factor in a number of unexplained illnesses, either upon primary infection or reactivation of latent virus. Because of the difficulty in identifying reactivation by antibody titers, RT-PCR detection of a gene expressed late in active infection will be used. The PCR assay will also distinguish and categorize EHV2 strains based on their extensive heterogeneity by use of restriction site differences within the amplified fragment. Reagents have been designed and tested for these experiments by the principal investigator while on sabbatical level. Upon optimization of the assay with *in vitro* reagents using the requested equipment from the grantee institution, the principal investigator will be in a position to apply for a NRICGP Seed Grant and/or Standard Research Grant for an epidemiological study assessing active EHV2 infection in

clinically relevant horse populations. Furthermore, the requested equipment will be used by at least two other members of the grantee department of research related to areas typically funded by USDA grants.

9703502 Modulation of Immune function in Young Pigs
Laurenz, J.C. **Grant 97-35204-4912**

Texas A&M University, Kingsville **Seed Grant**
Department of Animal and Wildlife Sciences **$25,000**
Kingsville, TX 78363-0156 **1 Year**

Mortality and morbidity associated with disease during the preweaning and early postweaning period continues to be a major problem facing the swine industry. Although there are many managerial and environmental factors that can contribute to these losses, the enhanced susceptibility of young pigs to disease is also reflective of the poor immunological status of the neonatal pig and the stress-induced suppression of immune function. With few exceptions, pigs are born having never been exposed to any diseases and are dependent upon the transfer of antibodies from the milk to acquire immunity (passive immunity). However, the sow also represents a major reservoir for disease exposure to the piglet. This paradox is the driving force for the use of early weaning programs in which the goal is to provide a time frame in which the piglet can obtain adequate nourishment and passive immunization from the sow, but be removed early enough to avoid exposure to disease. Yet, one of the biggest problems facing early weaning programs and cleaner, conventionally raised pigs is the losses that occur following weaning when young, high-health pigs are exposed to pathogens for which they have no immunity. Agents such as the branched #-1, 3-glucan (PCG-glucan) could provide a mechanism to increase antibody production by the sow, thereby, enhancing the period of passive immunization in the piglet. The specific aims of this research are to determine the effect of feeding PCG-glucan on: (1) antibody production by the sow, and (2) the extent of passive immunization of newborn piglets.

9703449 A Plant Growth Chamber to Enhance Research Activities in Plant Biology
Barnes, P.W. **Grant 97-35106-4799**

Southwest Texas State University **Equipment Grant**
Department of Biology **$16,771**
San Marcos, TX 78666-4616 **1 Year**

This project will fund the acquisition of a plant environmental growth chamber to support and enhance research activities examining the response of crop and rangeland plants to ongoing global environmental change. In particular, this growth chamber will allow for studies to be conducted on plants that are grown under very controlled conditions of temperature, visible light, ultraviolet radiation and carbon dioxide concentration. Thus, this chamber will significantly enhance ongoing, USDA-funded research examining the fundamental effects of stratospheric ozone depletion and increased solar ultraviolet radiation on crop plant growth and crop/weed competition. In addition, this chamber will be used in studies examining plant responses to changes in light, temperature and soil fertility that occur as woody plants, such as mesquite and juniper, invade and establish in landscapes that were historically grasslands or savannas. Finally, this growth chamber will support other research projects examining the reproductive biology of threatened and endangered plants, and the biology of insect herbivores and their associated host plants. Thus, this chamber will enhance a variety of research projects at Southwest Texas State University that are addressing topics such as stratospheric ozone depletion, brush encroachment of rangelands, conservation of plant genetic diversity, and insect-plant interactions which are especially relevant to agricultural productivity and sustainability.

9702337 Plant Activated Oxygen - Does It Affect Pseudomonads?
Anderson, A.J. **Grant 97-35303-5135**

Utah State University **Strengthening Award**
Biology Department **$118,769**
Logan, UT 84322-5305 **2 Years**

Leaf surfaces are colonized by bacteria, such as *Pseudomonas syringae* pv. *syringae* (Pss) B728a, that also have the potential to penetrate into the tissue and cause disease. Their survival is likely to require mechanisms of defense against the reactive oxygen species (ROS) that are generated as the result of sunlight interacting with the plant. The proposed studies will examine the role of expression of genes for the different isozymes of catalase and superoxide dismutase in their survival as leaf-associated organisms. Genes encoding the different isozymes of catalase and superoxide dismutase as well as a likely regulatory gene, rpoS , will be characterized in Pss B728a. Mutants lacking expression from each of these genes will be generated by gene disruption. The survival of the mutants will be tested in the susceptible host plant, bean (Phaseolus vulgaris). Survival as an epiphyte will be investigated in response to UV irradiation. Multiplication within the leaf tissue and extent of formation of the disease symptom of brown rot will be assessed. These studies will indicate whether specific isozymes of catalase or superoxide dismutase are crucial for the survival of the bacterium in the plant tissue.

703940 Fruit Bud Hardiness as Affected by Tree Rootstocks and Plant Growth Regulator Treatments
Anderson, J.L. **Grant 97-35311-4823**

Utah State University **Equipment Grant**
Department of Plants, Soils and Biometeorology **$14,230**
Logan, UT 84322-4820 **1 Year**

Deciduous fruit trees are subject to cold temperature injury during three stages of annual tree growth and development: in the fall during cold temperature acclimation, during midwinter, and in the spring during flowering. Rootstocks influence the winter hardening and dehardening processes. The freezing chamber purchased with this grant will be used to determine the cold temperature levels to kill apple, peach and cherry buds on terminal shoots and fruiting spurs. The differential hardiness of rootstocks and their influence on apple, peach and cherry scion cold hardiness will be evaluated through time as the trees acclimate and deacclimate to winter cold. This information is necessary before rootstocks can be recommended for trees in fruit production. The equipment will also be used to determine the effects of applied plant growth regulators on fruit tree bud hardiness and to obtain data on fruit tree cold temperature acclimation necessary to develop winter hardiness acclimation models for deciduous fruit trees.

9704007 Relationship Between Androgen Receptor Genotype and Epidemiologic Factors
Campbell, D.R. **Grant 97-35207-4619**

Utah State University **Seed Grant**
Department of Nutrition and Food Science **$49,487**
Logan, Utah 84322-8700 **2 Years**

The androgen receptor (AR) is involved in the regulation of sex hormone metabolism in men and women. Natural variations in the AR gene are associated with alterations in blood sex hormone levels and body shape. Both of these factors are related to three of the leading causes of death in the United States - cardiovascular diseases, diabetes, and two major cancers, i.e., prostate and breast cancers. Dietary intake is also associated with risk for these diseases.

It is unknown precisely how body shape, sex hormones, and dietary intake influence human disease risk. Interactions between genes and environmental factors are highly probable and require rigorous evaluation in relationship to disease susceptibility. If populations could be stratified on the basis of genetic characteristics, then relationships between various factors and metabolism or disease risk could be investigated. True risk factors may then be identified within specific genetic subsets of the population.

The purpose of this project is to investigate associations among AR genotype, body shape, blood sex hormone levels, and dietary intake in healthy older human adults. It is proposed that repetitive regions in the AR gene will vary in length in relationship to body shape and blood sex hormone levels; and that fruit and vegetable intake is associated with methylation density of the AR gene. Investigating associations among AR genotype and disease risk phenotypes will provide a better understanding of disease etiology. In addition, a genetic marker may be a sensitive and reliable marker of disease risk.

9703081 Preventing Mycotoxin Disease in Poultry by Dietary Induction of Glutathione S-transferases
Coulombe, R.A.; Buckner, R.E.; Frame, D. **Grant 97-35201-4959**

Utah State University **Strengthening Award**
Department of Animal, Dairy, and Veterinary Sciences **$163,802**
Logan, UT 84322-4620 **3 Years**

Mold-produced toxins are unavoidable contaminants of poultry feeds. Aflatoxin B1 (AFB1) is the most important mycotoxin with respect to occurrence and toxic potency, and poultry are the most susceptible food animals to it's effects. The annual economic impact of aflatoxin -related diseases to the poultry industry exceeds $100 million. Small amounts of AFB1 cause reductions in growth rate, feed efficiency, hatchability and increased susceptibility to bacterial and viral diseases. We have recently discovered that the extreme sensitivity of turkeys to AFB1 is primarily due to a deficiency of the toxin-fighting enzyme, glutathione S-transferase (GST). However, our studies have shown that, as with many mammalian species (including humans), the expression and activity of this important enzyme can be increased in turkeys by a simple addition of the FDA-approved antioxidant butylated hydroxytoluene (BHT) to the diet. We will confirm whether this and related dietary antioxidants shown to increase AFB1-detoxifying GSTs in mammals will do so in turkeys, and if these antioxidants will protect turkeys against AFB1-related toxicity. Because of the important role GST plays in protecting animals against both natural and synthetic toxins, we wish to characterize turkey GSTs. Dietary interventions with antioxidants and other chemoprotective agents is now recognized to be one of the most promising cancer-prevention strategies in people. Since AFB1 and other mycotoxins are unavoidable in feeds, discovering ways of protecting turkeys through simple dietary intervention with safe chemoprotective agents represents a practical management strategy that should be explored. Thus, our research will help to significantly reduce the losses associated with mycotoxins in poultry feeds, thereby helping the poultry industry to be more productive and to produce safer food for consumers.

9700593 Response of Canopy Photosynthesis to Turbulence-Induced Light Fluctuations
Hipps, L.E.; Bugbee, B. **Grant 97-35100-4502**

Utah State University **Strengthening Award**
Plants, Soils, and Biometeorology **$110,700**
Logan, UT 84322-4820 **2 Years**

Accurate models of CO_2 exchange in plant communities are essential for both agricultural concerns and for quantifying the role of vegetation in the carbon balance of the planet. The response of photosynthesis to light has been well studied. However, nearly all such studies have only considered steady-state or unchanging light conditions. In reality, turbulence causes rapid and complex fluctuations of light in plant canopies, often termed as sunflecks. Recent studies on individual leaves suggest that transient changes in light result in photosynthetic rates which differ from those under steady-state light values. Such investigations have never been conducted at the scale of a plant canopy. In addition, the present models for photosynthesis generally cannot and do not consider any effects of fluctuating light on CO_2 exchange. This study will integrate concepts and measurements from micrometeorology and plant physiology to measure the response of canopy photosynthesis to wind-induced light fluctuations. The CO_2 flux into the plant canopy will be measured and combined with measurements of the light regime inside the canopy. This will allow direct examination of the response of photosynthesis to the changing light conditions. In addition, a state of the art canopy model called CUPID will be run to simulate the CO_2 exchange for steady-state light conditions. Integrating the measurements with the model simulations will demonstrate whether fluctuations of light alter the photosynthetic rates, which would be predicted by current approaches.

9703769 Farm and Landscape Water Allocation and Conservation at the Rural:Urban Interface
Kjelgren, R.; Neale, C.; Endter-Wada, J.; Bishop, B. **Grant 97-35108-5123**

Utah State University **Strengthening Award**
Department of Plants, Soils, and Biometeorology **$246,357**
Logan, UT 84322-4820 **2 Years**

This project will investigate conservation strategies to reduce water transfer from agricultural to municipal and industrial uses in rural-urban interface areas. The water conservation potential both agricultural and urban amenity landscapes will be quantified and water conservation strategies will be designed based upon research of consumer, farmer, and water purveyor behaviors. Project personnel will work with local water management institutions and stakeholder groups to increase successful implementation of research findings.

Specific objectives are: predict total agricultural and irrigated landscaped area, using airbone multipsectroal videography; quantify woody plant water use coefficients as a function of reference evapotranspiration; estimate excess agricultural and urban landscape irrigation water applications for different canal command areas in the rural-urban interface; conduct social science research and involve relevant stakeholders to understand existing patterns of behaviors related to water use and to identify landscape and agricultural water conservation strategies that can be implemented.

9703491 Evaluation of Electroheating Technology for UHT Processing of Milk
McMahon, D.J.; Irudayaraj, J. **Grant 97-35501-4601**

Utah State University **Seed Grant**
Nutrition and Food Sciences Department **$49,976**
Logan, Utah 84322-8700 **2 Years**

This research will use electroheating technology for ultra-high temperature (UHT) processing of milk in collaboration with Raztek Corporation of Sunnyvale, California. The electroheating system design is unique in that it will allow the process to use heating rates and temperatures not attainable with conventional heat exchangers. It also eliminates the problem of milk coming into contact with hot surfaces because the heating takes place internally within the product. Also, it does not involve the introduction (and subsequent vacuum removal) of moisture into the milk inherent with steam injection systems. Past work on ohmic heating centered mostly on heating of particulate food materials such as vegetable and fruit juices, sauce, meat, and pasta products. None of the existing work was performed on milk; hence, there is no published information available on the physical, chemical, and microbial attributes of using electroheating for the ultra-high temperature processing of milk. Using electroheating, a process can be defined in which a shelf-stable milk can be obtained that has been heat-treated sufficiently to kill harmful microorganisms and inactivate the heat-resistant bacterial spores that are now becoming a problem to milk processors. Such a process would also allow for the production of milk with enhanced flavor, thus, making it suitable for use in the food service market. The main objective of this research is to obtain basic information on some functional, physical, and chemical properties of heated milk processed by electroheating. Recommendations will also be made for optimizing the process.

9703413 Impedance Analyzer (HA) for Electromagnetic Characterization of Soil Constituents at Low Frequencies
Or, D.; Dudley, L.; Harris, R. **Grant 97-35106-5057**

Utah State University **Equipment Grant**
Department of Plants, Soils, and Biometeorology **$18,500**
Logan, UT 84322-4820 **1 Year**

The requested Impedance analyzer (HP-4194A) offers a means for identifying, quantifying, and monitoring changes in soil constituents by measuring their different electromagnetic (dielectric) responses. Electromagnetic-based methods are powerful tools, as evident from the success of the time domain reflectometry (TDR) for measurement of water content and salinity. The objective of this study is to extend our understanding of low-frequency dielectric responses of soil constituents. The mechanisms involved in low-frequency dielectric response are quite different than those induced by high frequency methods such as TDR. The impedance analyzer would significantly improve our ability to study the relatively underdeveloped low-frequency dielectric spectrum emphasizing processes related to agricultural and environmental problems. Some of the advanced methods presently used for oil exploration (geophysics) could be adopted for *in-situ* characterization of soil electrochemical and geometrical properties. The analyzer would provide new insights into solid-liquid interfacial regions under unsaturated conditions where liquid is organized in thin films with vastly different electrochemical properties than inferred from saturated systems. The extension to field measurements should prove useful for studies on long-term organic matter accumulation with different tillage practices. The ability to monitor transport or macromolecules or colloid-facilitated translocation of pesticides should be greatly enhanced. These research aspects are compatible with the objectives of several NRI and USDA programs, and with the PI's long-term research interests. We believe that the availability of an impedance analyzer in our department and the potential results will enhance our competitiveness in pursuing future regular NRICGP proposals.

9700814 Post-tillage Soil Structure and Pore Space Dynamics
Or, D.; Snyder, V. **Grant 97-35107-4899**

Utah State University **Strengthening Award**
Department of Plants, Soils, and Biometeorology **$100,000**
Logan, UT 84322-4820 **2 Years**

The tilled "plow layer" of agricultural soils plays a crucial role in determining crop productivity and the transport of gas, water and chemical fluxes in the environment. A characteristic of this layer is the periodic disruption of soil structure by tillage followed by gradual resettling of the soil into more stable state. Two processes are considered fundamental: (i) fracture and breakdown of primary clods produced by tillage due to wetting and drying cycles; and (ii) subsequent rejoining of loose soil fragments into an increasingly cohesive soil mass of reduced porosity. The processes in turn determine temporal changes in transport properties through their effects on evolution of soil pore space geometry. The objectives of this study are to: 1) model primary processes governing aggregate fragmentation and rejoining following tillage; and 2) quantify effects of these phenomena on evolution of soil pore space and hydraulic properties. Soil swelling and fracture properties will be used to predict likelihood and extent of fragmentation due to cyclic and nonuniform wetting and drying. The theory of capillary-induced sintering of aggregated media will be used to model the fusing of wet soil fragments into larger and more stable structural units. The resulting till-dependent soil pore size distributions coupled with statistical models of hydraulic conductivity provide a means for quantifying changes in soil transport properties. The results should greatly enhance our understanding of the evolution of structure and associated hydraulic properties in tilled soils leading to improved precision management capabilities which are crucial to sustainable intensive agriculture.

9700599 Competition from native grasses for restoration of cheatgrass-infested range
Schupp, E.W. **Grant 97-35315-4926**

Utah State University **Strengthening Award**
Department of Rangeland Resources **$100,000**
Logan, UT 84322-5230 **2 Years**

The goal of our research is to develop a method to restore productivity to degraded weed-infested rangelands using native disturbance-adapted species to suppress weeds and promote succession to native rangeland. As a first step, the objective of this study is to investigate competition among the exotic weed cheatgrass, the disturbance-adapted native grass bottlebrush squirreltail, and the desirable long-lived native bluebunch wheatgrass during plant establishment. We use three-species mixed density plots with seeds of all three species sown together. Each experimental plot receives one of five densities of each species such that all possible combinations of densities are represented in the experiment (i.e., the lowest density of species 1 with all five densities of species 2 and of species 3). This is a powerful approach for measuring the effect of each species on growth, survival, and reproduction of the other species, and will help us understand the feasibility of using native disturbance-adapted species to help convert weed-infested rangelands to productive native rangelands. This research addresses a major problem in the western U.S.

and elsewhere; exotic annual grasses are a growing threat to economic productivity and ecological health of grazing lands worldwide. If viable, our strategy should provide substantial benefits to agriculture. Benefits to the livestock industry are two-fold. First, grazing land productivity and ecological condition will be improved, benefitting livestock directly. Second, by restoring native rangelands, some of the growing pressure for total livestock removal from public lands may be eased.

9703227 Prostacylcin Production by Uterine Arteries in Response to Lipopolysaccharide
Vagnoni, K.E. **Grant 97-35204-4912**

Utah State University **Strengthening Award**
Department of Animal, Dairy, and Veterinary Science **$140,000**
Logan, UT 84322-4700 **2 Years**

Anecdotal and clinical evidence suggest that female domestic animals vary in their response to noxious agents depending on the stage of their reproductive cycle. Exposure to one such noxious agent, lipopolysaccharide (the lipo-carbohydrate molecules which make up the cell wall of certain bacteria), commonly results in overreaction by the immune system (a condition called endotoxemia) which is often followed by abortion or death of the animal. Evidence exist for a regulatory role of the female sex steroid, estrogen, on the immune response to lipopolysaccharide. The research proposed in this study will determine the role of estrogen in regulating the response of sheep arteries to lipopolysaccharide. These studies will determine if estrogen's influence on immune response is limited to reproductive associated tissues (i.e., uterine arteries) or whether estrogen can influence tissue throughout the body (for example, arteries of the kidney). In addition, these studies will determine the cell population within arteries that respond to lipopolysaccharide. Data collected from these studies will provide useful information for determining the optimal timing for immunization of females and for better management of females once exposed to a noxious agent such as lipopoly saccharide. In addition, identification of the cell population which responds to lipopolysaccharide will provide useful information for development of vaccination and treatments which specifically target responding cells, thus increasing the effectiveness of these treatments. Taken together, data from these studies, when applied to management schemes, will allow further enhancement of animal health and well-being.

9703545 Effect Of Enhanced Protein Efficiency Of Dairy Cows On Manurial Nitrogen Excretion
Vagnoni, D.B.; Dhiman, T.R. **Grant 97-35208-4683**

Utah State University **Equipment Grant**
Animal, Dairy and Veterinary Sciences Department **$27,020**
Logan, UT 84322-4815 **1 Year**

Historically, livestock farmers in the United States have given little thought to excess nutrient excretion by their animals. Diets have been formulated for maximal production with less concern for the conversion efficiency of nutrients, and almost no regard for nutrient excretion per se. However, environmental consequences of excess nutrient excretion by livestock in general, and dairy animals in particular are receiving increasing attention. Whole-farm modelling analysis has indicated that the conversion of feed nitrogen to animal product nitrogen (e.g., milk) is the single most important factor affecting the environmental impact (through nutrient losses) of animal production operations. The funds awarded will be used to purchase a nitrogen analyzer that will allow us to determine the extent to which various dietary manipulations designed to enhance ruminal nitrogen metabolism and protein efficiency of lactating dairy cows will reduce the environmental impact of dairying by reducing manurial nitrogen excretion.

9700721 Watershed Scale Variability of Inorganic Nitrogen Dynamics in the Southern Appalachians
Van Miegroet, H.; Nicholas, N.S.; McCarthy, L.E.; Creed, I.F. **Grant 97-35101-3244**

Utah State University **Strengthening Award**
Department of Forest Resources **$291,000**
Logan, UT 84322-5215 **3 Years**

The high-elevation red spruce-Fraser fir forests in the Southern Appalachians leak large amounts of nitrate from the soil. This is thought to be the result of high nitrogen inputs from atmospheric pollution combined with a low capacity of the ecosystem to retain nitrogen. Such low nitrogen retention leads to high nitrate levels in the stream water which in turn deteriorate water quality. The high-elevation forests are quite heterogeneous with numerous gaps and large variations in stand age, the number of live and dead standing trees, and the amount of dead wood on the surface. Little is know about how important such spatial variability is to nitrogen retention in different parts of the watershed and ultimately to the overall nitrogen export from the catchment. This study will examine spatial differences in the release/retention of nitrogen within a 17.4-ha catchment located in the high-elevation spruce-fir forest of the Great Smoky Mountains National Park, its relationship to spatial patterns in forest structure and the distribution of dead wood, and its impact on streamwater nitrate levels. We hypothesize that the differences in N input with

elevation, in local forest structure, and in abundance and relative decay of dead wood causes significant but predictable variation in nitrogen release from soils across the watershed, with some areas acting as stronger nitrogen source areas than others. We will test this hypothesis through a combination of geographic information system and model-based watershed characterization, actual field measurement of nitrogen status of 50 plots located throughout a small watershed, and modeled vs. measured nitrate export from the watershed.

9701771 Interaction and Organization of Zeins in Maize Protein Bodies
Coleman, C.E. **Grant 97-35301-4222**

Brigham Young University **New Investigator Award/Strengthening Award**
Department of Botany **$100,000**
Provo, UT 84602 **2 Years**

Zeins are proteins produced in maize grain that are used by the seed to store nitrogen and amino acids for the germinating seedling. Approximately 50-60% of seed proteins are zeins. These proteins do not contain lysine or tryptophan, which are essential amino acids in the diet of humans, non-ruminant livestock and poultry. The reduced amount of these amino acids makes the grain nutritionally deficient. Zeins are packaged as spherical bodies within the cells of the seed's nutritive tissue. Disruptions in the way zeins are packaged lead to profound changes in the physical properties of the seed, all of which are detrimental to the commercial viability of the grain. It is the purpose of this project to study the interactions between zein proteins that lead to the formation of the spherical protein bodies. The project is also designed to learn whether the zein proteins can be altered, specifically by adding lysine and tryptophan amino acids, without significant interruption of their packing arrangement. These goals will be accomplished by transferring normal and altered forms of the zein genes into tobacco plants. Interactions between the zein proteins in the seeds of these tobacco plants can then be studied without interference from native proteins. The results from these experiments will provide a basis for future work of genetically introducing modified zein proteins into maize seeds in order to manipulate the balance of amino acids.

9701391 The Plant Mitochondrial *nad1* Gene/*mat-r* Gene Complex
Wolstenholme, D.R. **Grant 97-35301-4689**

University of Utah **Strengthening Award**
Department of Biology **$100,000**
Salt Lake City, UT 84112-0840 **2 Years**

The gene (*nad1*) for subunit 1 of the mitochondrial NADH dehydrogenase complex (complex I of the respiratory chain) of maize is interrupted by four introns of the group II kind. One of these introns contains a gene (*mat-r*) for a protein related to yeast group II intron maturases, and this intron and two others are themselves interrupted by large sequences that include other genes. Consequently, different segments of the *nad 1* gene (exons) and the associated half introns are separately transcribed. It is postulated that these transcripts must join either by hydrogen bonding between complimentary sequences, or by end-to-end covalent linkage to generate complete group II introns that can be correctly excised to produce functional transcripts. We propose to define the exact ends of transcripts that contain the two halves of each split intron in order to determine what sequences could be included in the reassociated intron, and whether observed, short repeated sequences might mark the locations at which the intron sequences were divided by recombination. A further series of experiments will be carried out to determine whether it is likely that *trans*-splicing of split introns and *cis*-splicing of the fourth, continuous intron of the maize *nad1* gene follow a similar pathway to that of yeast mitochondrial and plant chloroplast group II introns that are known to involve a lariat-like intermediate.

9703915 Analysis of Somatic Mutations Induced by Specific Immune Responses in Trout
Kaattari, S. L. **Grant 97-35205-5130**

College of William and Mary Virginia Institute of Marine Science **Strengthening Award**
Department of Environmental Sciences **$162,000**
Gloucester Point, VA 23062-1346 **2 Years**

The exquisite specificity and affinity of antibodies for invading pathogens is essential to the induction of protective immunity. An essential element in the acquisition of these high affinity antibodies is the process of somatic mutation. During an immune response, mutated antibody-producing cells which possess the highest affinity for the pathogen become predominant among the responding lymphocytes, resulting in a shift to the production of more highly specific antibodies. This process of somatic mutation is well-characterized in mammals, but has only been observed recently in fish. Thus far these few reports in fish have not addressed the role of somatic mutation in the development of specific immune responses. It is the purpose of this study to examine the role of somatic mutation in the development and maturation of the protective antibody response to the salmonid pathogen, Infectious Hematopoietic Necrosis Virus (IHNV). Our studies will be focusing on the antibody response to the surface

glycoprotein (G) of IHNV, which can confer protective immunity. Past work in mammals indicates that somatic mutations occur in response to protein antigens. Thus, this study uses a protein antigen, not only as a general immunological model protein, but one which has direct application to disease resistance in trout. It is anticipated that we may be able to derive knowledge of the conditions that are essential to the formation of the highest affinity antibodies to viral pathogens, and use this knowledge to develop more efficacious vaccine methodologies.

9701881 China's Urban Consumer Demand for Livestock Products and Edible Oils Implications for U.S. Export
Halbrendt, C.; Wang, Q. **Grant 97-35400-4437**

University of Vermont and State Agricultural College **Strengthening Award**
Department of Community Development and Applied Economics **$115,000**
Burlington, VT 05405 **2 Years**

This study analyzes the changes in China's urban consumer demand for livestock products and edible oils and assesses the potential impacts of such changes on U.S. food exports to China. U.S. agricultural trade balance with China reversed from a deficit of $74 million in 1993 to a surplus of $2,154 million in 1995 and this significant turnaround is important for the U.S. to narrow its overall trade deficit with China. As China moves towards a market economy, its institutional trade barriers are declining and food trade behavior is increasingly dependent on consumer demand. It is becoming more important for U.S. exporters to understand the underlying economic and cultural factors of the Chinese markets, this study focuses on urban demand because urban residents are the primary consumers of China's imported food products and their proportion in China's total population has increased from 18% in 1978 to 30% in 1995. A consumer survey will be conducted in three Chinese cities with the assistance of our Chinese collaborators and quantitative demand models will then be used to analyze the impacts of economic and cultural factors on consumer food demand and preference for imported food products. Three major results are expected from this study; a detailed database of Chinese urban consumption of livestock products and edible oils and information on consumer valuation of imported food products, estimates of demand elasticities and sociodemographic effects for individual food commodities, and information that can be used to develop effective marketing strategies to promote U.S. food exports to China.

9703557 Beckman Elutriation System Equipment Grant
Brown, W.C. **Grant 97-35208-4724**

Washington State University **Equipment Grant**
Department of Veterinary Microbiology and Pathology **$24,089**
Pullman, WA 99164-7040 **1 Year**

The Beckman Elutriation System will be used by several investigators for the purification of viable cells in a non-activated state. One major application of this equipment will be the purification of large numbers of non-activated monocytes and macrophages from peripheral blood or lung ravage of large domestic animals, including cattle, goats, sheep, and horses. This will facilitate the investigation of T cell-antigen presenting cell (APC) interactions and the regulation of APC function by cytokines. For example, we will determine the effects of the macrophage deactivating cytokine, IL-10 on the induction of the costimulatory surface molecule B7, MHC class 11 required for antigen presentation, and expression of the inflammatory cytokine IL- 1 2 in monocytes. A second major application will be the purification of hemoparasite-infected erythrocytes from culture or peripheral blood of animals infected with *Babesia bovis, Babesia bigemina, Babesia equi, or Anaplasma marginale*. We have identified many CD4+ T helper cell clones that recognize unique protozoa, (*Babesia bovis, Babesia bigemina*) or rickettsial (*Anaplasma marginale*) determinants, and express the macrophage activating cytokine IFNy. We will study the effects of hemoparasite-specific T cells that produce IFNy and of IFNy-activated macrophages on the viability of *Babesia* or *Anaplasma*. Specifically, we will determine: (1) whether IFNy-activated macrophages will kill or inhibit hemoparasite growth; (2) the molecular mechanism for hemoparasite growth impairment, and (3) the parasite products that induce macrophage products potentially important for killing *Babesia* or *Anaplasma*, such as nitric oxide (NO) and TNF+, or for modulating the host immune response, such as IL-10, and IL-12.

9704061 Flow Cytometer Acquisition
Byrne, K.M.; Leid, R.W.; Ristow, S.D.; Mirando, M.A.; Chew, B.P.;
Dodson, M.V. **Grant 97-35208-4721**

Washington State University **Equipment Grant**
Department of Animal Sciences **$49,719**
Pullman, WA 99163-6351 **1 Year**

This proposal received matching funds to acquire a flow cytometer. A flow cytometer is a very versatile piece of equipment which enables researchers to rapidly identify different populations of cells in a sample. This is particularly important to the study of cells of the immune system where a change in population of cells can lead to either health or disease depending on which

population of cells has increased. Researchers involved in this grant will be using the flow cytometer to identify cytokine expression in cells in muscle and reproductive tissue, characterize the types of lymphocytes responding to viruses, analyze the surface expression of receptors important for reproduction, study the impact of diet on tumor gene expression, and differentiate populations of cells involved in muscle regeneration.

9702111 Incompatibility Genes of the Stored Product Pest, Tribolium castaneum
Thomson, M.S. **Grant 95-37311-2399**

University of Wisconsin, Parkside **Strengthening Award**
Biological Sciences **$57,000**
Kenosha, WI 53141-2000 **2 Years**

The red flour beetle is a pest of stored grain and other food products world-wide. Our research focuses on breeding relationships within the species. Numerous laboratory strains, each of distinct geographic origin, are maintained by the principal investigator. Hybrids produced by mating males and females from different strains are generally healthy. In contrast, hybrids of certain strains are defective. These die as larvae or develop to adults that are infertile, have poorly developed gonads, have poor muscular control, and are short-lived. This phenomenon is called hybrid incompatibility. Genetic analysis of hybrid incompatibility in other plants and animals has revealed a diversity of underlying mechanisms. Such studies enrich our understanding of the genetic mechanisms driving evolution. Some of these have led to powerful methods of genetic manipulation and engineering. We have already identified two incompatibility genes in flour beetles: H, and an incompletely described family of genes called Medea factors. Incompatibility results when H and one of the Medea factors are combined in the same individual. The precise nature of incompatibility varies with Medea factor. Our goal is to continue genetic analysis of this system, including: complete characterization of the interactions between H and Medea; identification of genes that modify the interaction of H and Medea; development of efficient techniques to observe these genes in natural populations, and assessment of the similarity of flour beetle incompatibility to this phenomenon in other species. The knowledge gained will enhance general understanding of insect evolution and genetics, and support practical methods for managing insect populations.

9703419 The Effect of Mycorrhizal Fungal Interactions on Plant Growth
Bentivenga, S.P. **Grant 97-35106-4802**

University of Wisconsin, Oshkosh **Seed Grant**
Department of Biology and Microbiology **$49,993**
Oshkosh, WI 54901-8640 **2 Years**

Most plants growing in either managed or native ecosystems receive assistance in inorganic nutrient acquisition by symbiotic soil fungi, called arbuscular mycorrhizal (AM) fungi. In nature, one individual plant usually is colonized by several genetically distinct AM fungi (i.e., different species or strains). The net effect of the symbiosis on plant growth is undoubtedly related to the combined effect of all colonizing AM fungi in concert. However, our knowledge of how different fungal species and strains interact to influence plant growth remains unclear. Research will be performed that will examine the interactions between different AM fungal isolates, and their combined impact on plant growth. Using a technique called a replacement series, carefully defined ratios of two different AM fungal isolates will be used to inoculate plants. Plant growth, mycorrhizal colonization, and AM fungal sporulation will be measured to determine the effect of the various fungal combinations. Information gained from these experiments will lead to a better understanding the potentially complex interactions between mycorrhizal fungal strains and species. The information gained will lead to a better understanding of the complexities of the symbiosis in native and agronomic ecosystems. Understanding the intricacies of AM fungal populations represents an important step towards developing culturing and inoculation strategies, so that mycorrhizal fungi can be predictably manipulated in agronomic and horticultural systems.

9703420 Application of a Modern Ultramicrotome to Plant Physiology Research
Wise, R.R. **Grant 97-35311-4824**

University of Wisconsin, Oshkosh **Equipment Grant**
Department of Biology and Microbiology **$18,657**
Oshkosh, WI 54901-8640 **1 Year**

Every biological function has at its foundation a physical structure. The research program for which this proposal seeks funding lies at the intersection of function and structure in modern plant biology. Two specific research projects are currently underway in the P.I.'s laboratory. Both projects are studying chloroplasts, the organelles found in plant leaf cells that are responsible for photosynthesis. The first project uses various modes of electron microscopy and image reconstruction to resolve the three-dimensional structure of the chloroplast internal membrane system. This novel 3-D model will be used to test theories of photosynthetic electron transport. To date, such investigations have only been able to consider electron transport in two dimensions. The second project is investigating the effect of environmental stress (chilling injury) on the positioning of

chloroplasts within leaf cells. The primary focus is on the physiology of the chloroplast motile system (the cytoskeleton) and the energy supply needed to fuel the movement (ATP supplied by respiration). Light and electron microscopy are being used to track the position of chloroplasts during these experiments. The instrument funded by this proposal, an ultramicrotome, is used to prepare biological samples for viewing in both the transmission electron microscope and light microscope and is vital to the success of both of the projects described above. The procurement of a new, modern ultramicrotome will allow the P.I. to pursue these projects and to continue to seek external research funding.

9700808 Ecotypic Variation in Ectomycorrhizal Fungi from Serpentine Soils
Cumming, J.R.; Panaccione, D.G. **Grant 97-35107-4374**

West Virginia University **Strengthening Award**
Department of Biology and Division of Plant and Soil Sciences **$190,000**
Morgantown, WV 26506-6057 **3 Years**

Mycorrhizal fungi form a uniquely beneficial symbiotic relationship with the roots of trees. These fungi increase nutrient uptake and environmental stress tolerance of their tree hosts. To date, little is known of the specialization within these fungi with respect to soil chemical characteristics. The overall goals of this research are to determine the extent to which the chemistry of soils influences populations of these fungi and to elucidate the mechanisms of stress tolerance in these fungi that function to protect trees from toxic metals in the environment. Naturally-occurring serpentine soils in Lancaster County, PA, characterized by elevated magnesium and nickel concentrations, will be used in these investigations. Genetic studies will utilize DNA fingerprinting to analyze biodiversity in populations from serpentine and non-serpentine environments. Physiological studies will investigate metal tolerance systems in fungi, including those based on metal detoxification in the soil and within fungal tissue. Finally, the capacity of fungi to confer metal tolerance to Virginia pine seedlings will determined. Together, these studies will indicate whether soil factors are influencing biodiversity in these fungi, what physiological mechanisms are selected for in these soils, and may lead to the identification metal tolerant individuals. Although serpentine soils are relatively rare in the United States, these sites provide a unique opportunity to study the biodiversity and physiology of stress tolerance in mycorrhizal fungi. Isolation and identification of mycorrhizal genotypes tolerant of metals may provide an aid to the reforestation and reclamation of mined or pollution-contaminated lands.

9702405 Mechanisms of *Streptococcus suis* Meningitis
Drevets, D.A. **Grant 97-35204-4486**

West Virginia University R.C. Byrd Health Sciences Center **Strengthening Award**
Department of Medicine **$110,000**
Morgantown, WV 26506-9163 **2 Years**

Streptococcus suis is pathogenic bacterium found in swine herds throughout the world for which an effective vaccine is not yet available. It is a major cause of severe infections in young swine including sepsis, serositis, and meningitis. One mechanism used by microbes to invade protected spaces such as the central nervous system is for circulating bacteria to bind vascular endothelial cells and then enter them. Bacterial infection of endothelial cells in turn stimulates a host response including production of pro-inflammatory cytokines and upregulated expression of endothelial cell adhesion molecules. Current models of bacterial meningitis show that these responses are critical for enabling leukocyte recruitment and entry into the central nervous system. Despite growing knowledge of inflammatory mediators and leukocyte endothelial cell adhesion mechanisms, little information exists about basic mechanisms of inflammation in *S. suis* meningitis. In this project we will characterize production of pro-inflammatory cytokines systemically and in the brain during experimental *S. suis* infection. We will test whether the expression of specific brain microvascular endothelial cells in vitro, and determine whether endothelial cell infection alters their adhesion molecule expression or their adhesiveness for neutrophil and monocytes. The in depth study of the host response to this bacterium may ultimately lead to opportunities to intervene in the disease process though drugs other than antibiotics, or by identifying new targets for vaccine development.

9700671 Investigating the Variable Response of Forest Watersheds to Chronic N Deposition
Peterjohn, W.T.; Cumming, J.R. **Grant 97-35101-4794**

West Virginia University **Strengthening Award**
Department of Biology **$217,000**
Morgantown, WV 26506-6057 **3 Years**

Chronic additions of nitrogen by acid deposition may eventually exceed the capacity of a forest to utilize this nutrient - a condition known as nitrogen saturation. Once this capacity is exceeded, the excess nitrogen may degrade water quality, reduce soil fertility, alter the release of greenhouse gases, and contribute to forest decline. Several studies have noted, however, that not all forests receiving elevated inputs of atmospheric nitrogen show symptoms of nitrogen saturatio The factors

responsible for the variable response of forests to high nitrogen inputs are currently unknown and are the focus of this study. In this project, we will compare two forested watersheds that are similar in their age, climate, geology, land-use history, and nitrogen deposition regime. Yet, despite their similarities, the concentration of inorganic nitrogen in stream water leaving these watersheds differs by a factor of two. To identify factors that are associated with the different behavior of these watersheds, we will measure a variety of soil, microbial, and plant variables that may account for their different abilities to retain inorganic nitrogen. Results from this study will test our current understanding of nitrogen saturation, expand the existing long-term data set for these watersheds, and will help us identify characteristics that make some forests more resistant to nitrogen saturation.

9702532 Coleopteran Receptors for *Cry3* Toxins from *Bacillus thuringiensis*.
Bulla, L.A.; Francis, B.R. **Grant 97-35302-4781**

University of Wyoming **Strengthening Award**
Department of Molecular Biology **$110,000**
Laramie, WY 82071-3944 **2 Years**

Parasporal crystals produced by particular subspecies of the gram positive bacterium, *Bacillus thuringiensis*, are toxic to insect larvae. The crystal proteins are believed to be proteolytically cleaved in the larval midguts to produce the toxins, which are referred to as *Cry* toxins. *Cry3* toxins are specific for beetle larvae. Toxicity by *Cry3* toxins is believed to be mediated by binding to beetle midgut receptors but only a *Cry3A* binding protein in mealworm larvae has been reported. The long-term goals of this research are to identify and characterize the receptors in beetle midguts for *Cry3* toxins and to understand how the interaction of toxins with these receptors leads to toxicity. The specific objective of this research is to identify and compare the high affinity receptors in the mealworm *Tenebrio molitor*, the southern corn rootworm *Diabrotica undecimpunctata howardi* and the Colorado potato beetle *Leptinotarsa decemlineata* for *Cry3A, Cry3Ba and Cry3Bb* toxins. Important economic benefits can be derived from the biological control of rootworms and potato beetles using *Cry3* toxins. Determining what the receptors are for *Cry3* toxins is a first step to understanding how beetle-specific toxins bind to midgut receptors. This in turn should allow new toxins to be produced that enable the effectiveness of the toxins as control agents to be maintained and even increased.

9702406 Uterine Chemokines
Hansen. T.R.; Perry, D.J. **Grant 97-35203-4808**

University of Wyoming **Strengthening Award**
Department of Animal Science **$130,000**
Laramie, WY 82701 **3 Years**

Pregnancy is dependent upon a receptive uterus which allows attachment and invasion of the conceptus while preventing immunological rejection. Uterine proteins (8-kDa) are secreted in response to interferon-tau (IFN-tau) during early pregnancy in the cow. Amino acid sequencing of four internal peptides revealed identity with the alpha chemokine family: bovine (b) granulocyte chemotactic protein-2 (GCP-2; 92-100% identity), and murine (m) macrophage inflammatory protein-2 (mMIP-2 (67-88% identity). Use of polyclonal bGCP-2 peptide antiserum in Western blot studies revealed that bGCP-2 is secreted by the endometrium during early pregnancy in response to conceptus-derived IFN-tau, and not during the estrous cycle or in response to the closely related IFN-alpha. Chemokines are potent chemo-attractants for cells of the immune system and have been implicated in inflammatory and angiogenic processes. We hypothesize that IFN-tau and the alpha chemokines alter secretion of endometrial cytokines to a humoral (T helper 2, TH2) rather than a cell-mediated (T helper l, TH1) phenotype. The chemokines may attract conceptus trophoblast and/or immunocytes to implantation sites where a directed immunostimulatory phenotype (TH2) coupled with scavenger effects (macrophage, neutrophils) would control inflammatory and angiogenic invasion of the maternal endometrium by the conceptus trophoblast.

Purified native uterine alpha chemokines and rbIFN-tau will be used to determine if they induce release of TH2 cytokines (i.e., interleukin (IL)-4 and IL-10) by cultured endometrial explants and peripheral blood lymphocytes. Alpha chemokines also will be tested for the ability to attract granulocytes, monocytes and trophoblast cells in a chemotactic bioassay. The bMIP-2 amino acid sequence is not known. Thus, uterine alpha chemokines will be examined further for amino acid sequence identity. The bGCP-2 peptide antiserum will be used to identify endometrial cells expressing the protein. The bGCP-2 cDNA will be isolated, sequenced and used as a probe to study transcription of bGCP-2 mRNA in endometrium during early pregnancy. Identification of the alpha chemokines in the uterine endometrium is novel. Also, the alpha chemokines represent the first novel markers of IFN-tau-specific action. The proposed experiments are the first to examine the IFN-tau/alpha chemokine system during early pregnancy.

9703469 Equipment to Enhance Research Capability in Department of Veterinary Sciences
Raisbeck, M.F. **Grant 97-35208-4815**

University of Wyoming **Equipment Grant**
Department of Veterinary Sciences **$12,500**
Laramie, WY 82070 **1 Year**

This grant is intended to purchase an ultrasonic nebulizer (Cetac U6000AT or equivalent) to enhance the research capabilities of the University of Wyoming Department of Veterinary Sciences. Specifically the equipment will be used in conjunction with an existing inductively coupled argon plasma spectrometer. This piece of equipment leverages existing research capabilities and programs, notably toxic and nutritional problems of domestic livestock and environmental problems associated with irrigation, by increasing the sensitivity and reproducibility of an existing piece of equipment. This, in turn, should help the faculty of this department and their collaborators be more competitive in future proposals.

9702154 Regulation of viral and viral pathogenesis by pPKR
Roth, D. **Grant 97-35303-5104**

University of Wyoming **Strengthening Award**
Department Molecular Biology **$118,769**
Laramie, WY 82071-3354 **2 Years**

Understanding the mechanisms by which the infection processes of plant viruses and viroids are regulated is fundamental to developing rationale disease management strategies. Although many aspects of host-pathogen interactions have been examined in plants the consequences of infection on protein synthesis remain unclear. In eukaryotes, control of protein synthesis provides a rapid and reversible mechanism regulating cell response to diverse stresses, pathogenesis, growth and differentiation. A central pathway for translational control in mammals involves the phosphorylation of initiation factor 2a (elF2a) by the dsRNA stimulated protein kinase PKR. This signal transduction pathway has also been discovered in plant cells. Our hypothesis is that infection differentially and/or locally alters protein synthesis and that this conditions the ability of the pathogens to successfully infect cells.

The objectives of this grant are to characterize central Components of this regulatory framework ant determine the functional consequences in infected plants. Specifically, plant PKR, eIF2a phosphorylation and protein synthesis levels will be determined in response to virus and viroid infection. In addition, individual components of the pathway will be manipulated in transgenic plants and the resultant effects on pathogenesis evaluated. Characterization of the key targets of viral and viroid induced translational control and understanding their involvement in pathogenesis is prerequisite to developing approaches to manipulate their activity to increase plant resistance. Preliminary evidence suggests that diverse viruses and viroids affect the normal function of the plant PKR mediated pathway, thus, broad spectrum resistance to multiple pathogens may be possible by this approach.

9702896 Lateral Load Behavior of Traditional Timber Frames
Schmidt, R.J. **Grant 97-35103-5053**

University of Wyoming **Strengthening Award**
Department of Civil and Architectural Engineering **$79,500**
Laramie, WY 82071-3295 **2 Years**

This research project focuses on the behavior of traditional timber frame structures under the effects of lateral load. Traditional timber frames rely entirely on wood joinery and wood peg connections to resist load. Current building codes and design specifications do not address the use of wood fasteners, do not adequately describe the observed failure mechanisms in these connections, and do not contain provisions for load sharing between the structural frame and its typical enclosure system. The goal of the proposed research is to develop mathematical behavior models that accurately represent the strength and stiffness of traditional timber frames. The research program will be conducted through experimental studies of joint assemblies and full-scale structural frames. Successful completion of this research is expected to expand the market for traditional timber frame structures, to improve utilization of wood resources through more efficient design, and to improve safety of the occupants of these structures.

POSTDOCTORAL FELLOWSHIPS

Postdoctoral Fellowships are available to individuals who have recently received their doctoral degree and are initiating an independant research program under the guidance of an established investigator. Awards are made directly to the individual and are primarily for salary support. Postdoctoral Fellowships are reviewed in the program area most appropriate for the type of research proposed; therefore, these nontechnical summaries also appear under the respective program areas.

9703000 Effects and Dynamics of *Wolbachia* in the Fire Ant *Solenopsis invicta*
Shoemaker, D.D. **Grant 97-35302-5102**

University of Arizona **Postdoctoral Fellowship**
Department of Entomology **$90,000**
Tucson, AZ 85721-0106 **2 Years**

The introduced fire ant *Solenopsis invicta* has become a significant economic, medical, and agricultural pest in the southeastern USA since its introduction 60 years ago. Attempts to control introduced fire ants, however, essentially have been unsuccessful and these ants continue to persist at high population densities and to expand their range throughout the southern USA. The main goal of my project is to evaluate *Wolbachia*, a group of maternally-transmitted bacteria infecting the reproductive tissues of insects, as a potential biological control agent of introduced fire ants. These microbes are known to have or induce a number of phenotypic effects on insects that may be exploited for suppressing or controlling insect populations. I will study native fire ant populations infected with *Wolbachia* to determine the frequency and distribution of this microbe in native fire ant populations, the fidelity of maternal transmission of *Wolbachia* in fire ants, and the phenotypic effects of *Wolbachia* on fire ants. These studies are important because we now have the unique opportunity to examine the effects of a potentially significant biological control agent on a naturally infected population of a major pest species. Indeed, these studies are essential for further understanding the population dynamics and effects of *Wolbachia* in natural host populations as well as determining the prospects that such microbes can become biological control agents of fire ants in an integrated management scheme.

9702917 Argentine Ants in Their Native Habitat: Effects of Diversity, Competition, and Parasitism
Orr, M.R. **Grant 97-35302-4965**

University of California, Berkeley **Postdoctoral Fellowship**
Department of Environmental Science, Policy, and Management **$90,000**
Berkeley, CA 94720 **2 Years**

The Argentine ant (*Linepithema humile*) is native to South America and in recent years has invaded sites across the world. In the United States, it eliminates virtually every other native ant species in certain natural habitats, which in South Africa has been shown to have repercussions for the plant community due to the specific roles that different ant species play in dispersing seeds. The Argentine ant also is a ubiquitous pest in agriculture, where it tends and protects crop pests such as aphids. Preliminary research indicates that the abundance of Argentine ants in Brazil relative to other ant species diminishes in areas where there occurs a parasitic fly (family Phoridae, or Phorid fly) that attacks only Argentine ants. This fly is absent in all of the Argentine ant's introduced range. Preliminary research also demonstrates that Argentine ants abandon foraging and return underground in the presence of their phorid fly parasites. The goal of the proposal is to better understand the ecology of Argentine ants in their native habitat by (1) measuring the diversity of ant species that co-occur with Argentine ants in South America; (2) evaluating the relative influence of phorid flies and competing ant species on the ability of Argentine ants to gather food resources; and (3) studying the development and host specificity of phorid fly parasites of Argentine ants. Overall, the research may not only reveal novel mechanisms that regulate ant populations, but also provide sustainable solutions for controlling populations of pest ants.

9702996 Mechanisms of Competitive Dominance in the Invasive Argentine Ant
Holway, D.A. **Grant 97-35302-4920**

University of California, San Diego **Postdoctoral Fellowship**
Department of Biology **$90,000**
La Jolla, CA 92093 **2 Years**

The Argentine ant (*Linepithema humile*) is a highly invasive species that competitively displaces native ants throughout its expansive introduced range. In part due to its strong competitive ability, the Argentine ant is an important agricultural and household pest in California and parts of the southeastern United States. Despite its pest status, little is known about the biology of this species. The work described here seeks to isolate those mechanisms most responsible for the Argentine ant's strong competitive ability.

This proposal will test how different aspects of the Argentine ant's colony structure determine its competitive proficiency. The first objective will be to test how colony size (number of workers) and spatial structure (number of separate nests) affect the ability of colonies to takeover, defend, and harvest resources. The second objective will be to assess the degree to which colonies relocate nests to move them closer to food. The third objective will be to determine the degree to which workers in separate nests communicate with one another in the context of foraging decisions. These aspects of colony structure have never been studied in as much detail.

A better understanding of the Argentine ant's competitive ability will prove essential to control efforts. Strategies directed at those attributes responsible for its prowess as an invader will stand the best chance of mitigating the effects of these invasions.

Moreover, such knowledge will directly relate to the control of other ant invasions, since many invasive ant species (including the imported fire ant, *Solenopsis invicta*) possess a colony structure similar to that of the Argentine ant.

9701919 Inter-organelle Communication: Signals and Transcription
Larkin, R.M. **Grant 97-35301-4656**

The Salk Institute for Biological Studies **Postdoctoral Fellowship**
Plant Biology Laboratory **$75,000**
La Jolla, CA 92037 **2 Years**

The functional state of the chloroplast affects the transcription of nuclear genes that encode chloroplastic proteins, but the molecular nature of chloroplast-to-nucleus communication is not known. The goal of the proposed research is to identify chloroplastic signals that control nuclear gene transcription and to gain insight into the mechanism of repression of nuclear gene transcription in cells that contain chloroplasts that have been inactivated by photooxidative damage (photobleaching). Biochemical experiments have been designed to identify a factor that affects nuclear gene transcription and responds to the functional state of the chloroplast. The biochemical properties of a factor(s) that is identified by this approach will be studied. These biochemical studies will provide information that will be useful for isolating the gene(s) that encodes this factor. The proposed research will also involve the study of previously identified mutations in one of six nuclear genes (referred to as *gun* for genomes uncoupled) that impair the repression of nuclear gene transcription in photobleached cells. The GUN4 protein is thought to interact with two other GUN proteins or to function in a redundant signaling pathway. Moreover, *GUN4* and other *GUN* genes appear to perform non-overlapping functions during the plant life cycle. Thus, *GUN4* is an important component of this inter-organelle signaling pathway. Experiments have been designed to isolate the *GUN4* gene by genetic methods. The combined biochemical and genetic approaches should help to illuminate molecular mechanisms of chloroplast control of nuclear gene transcription.

9700889 Assessing a Volume of Weed Influence for Various Weed-Crop Canopy Architectures.
Steinmaus, S.J. **Grant 97-35315-4788**

University of California, Riverside **Postdoctoral Fellowship**
Botany and Plant Science Department **$85,000**
Riverside, CA 92521 **2 Years**

The angles and locations of leaves on a plant are characteristics that describe plant canopy architecture. These characteristics determine light interception and, thus, photosynthesis and growth. In situations where light is limiting to growth, common in agroecosystems, leaf angle and area distribution are reliable predictors of weed and crop competitive outcomes. The primary objective is to quantify the 3-dimensional distribution of leaf area and orientation for weed and crop foliage under competitive conditions. This will assist in understanding weed-crop competition for light and the effect of canopy architecture on light interception. The fundamental challenge until recently has been to describe the distribution of foliage for each species in a 3-dimensional sense because of the labor intensive methods required to acquire such data. My preliminary data describes these distributions for a single species utilizing recently available technologies. Thus, I propose to define a 'volume of weed influence' to assess weed impacts on overall crop photosynthesis. A 'volume of weed influence' for different weed canopy types will be incorporated into an existing weed-crop competition computer simulation, INTERCOM. The model will assist in predicting the canopy characteristics that make weeds competitive. This information could assist breeders in crop improvement programs. For example, crop varieties typically do not respond to the presence of neighboring plants. This work might suggest ways by which a crop is made more competitive against weeds, and thus reduce herbicide requirements.

9701293 Elucidation of the Programmed Cell Death Program in Developing Maize Endosperm
Young, T.E. **Grant 97-35304-4657**

University of California, Riverside **Postdoctoral Fellowship**
Department of Biochemistry **$82,000**
Riverside, CA 92521-0129 **2 Years**

During maize kernel development, the endosperm undergoes a cell death program such that at maturity, the endosperm is comprised of non-living starchy endosperm cells surrounded by a single layer of living cells which have differentiated into the aleurone layer. I have carried out preliminary analyses to characterize programmed cell death (pcd) in maize endosperm and found that cell death initiates within the central endosperm and progresses from the cap toward the base as the endosperm matures. The onset of pcd is preceded by an increase in ethylene synthesis. During cell death, the DNA underwent internucleosomal fragmentation, a hallmark of apoptosis. Ethylene treatment of developing kernels promoted these characteristics of cell death, whereas treatment with an inhibitor of ethylene biosynthesis reduced them, suggesting that ethylene may play a role in triggering the onset of pcd in developing maize endosperm. I will begin the elucidation of steps in the ethylene signal transduction pathway by isolating the ACC synthase gene(s) to use as a tool to identify factors responsible for regulating its expression. I will also isolate

the gene(s) encoding the nuclease responsible for the pcd-associated DNA fragmentation to use as a tool to identify intermediate steps in the endosperm pcd process. These studies will provide a starting point to understand the mechanisms responsible for pcd during maize kernel development and may lead to our ability to improve endosperm quality and yield by increasing endosperm life.

9703656 Endocrine Correlates and Nutritional Constraints on Environmental Adaptation and Growth in the Euryhaline Tilapia, *Oreochromis mossambicus*
Shepherd, B.S. **Grant 97-35206-5904**

University of Connecticut **Postdoctoral Fellowship**
Biotechnology Center **$90,000**
Storrs, CT 06269 **2 Years**

The Tilapia, *Oreochromis mossambicus*, which will be the focus of our studies, is an economically important finfish. The assent of tilapia aquaculture makes it inevitable that efforts will be directed toward the development of technologies to increase the growth of these fish to enhance production. Our objective is to develop a better understanding of how environmental salinity and nutrition interact to affect the hormones which regulate growth and adaptation in different environmental salinities. There are several metabolic processes in an animal that are necessary for adaptation and growth in an aquatic environment. Of the processes involved, the maintenance of salt and water balance (osmoregulation) is essential to life. To study osmoregulation one must also study growth since these two processes require considerable energy and are regulated by the same hormones (Growth Hormone: GH and Prolactin: PRL). The effects of GH on growth and of PRL on osmoregulation are well characterized in fishes; however, the effects of PRL on growth and of GH on osmoregulation are not. Our limited understanding of actions of GH and PRL in these processes is further complicated by findings that Insulin and the Insulin-like growth factors (IGF-I and -II) are involved in mediating some of the actions of GH and PRL, and that these intermediaries are themselves altered by environmental and nutritional factors. The aim of this study, therefore, is to clarify the roles that GH, PRL and their mediators (IGFs) play in the nutrition, growth and adaptation of tilapia to different environmental salinities.

9700561 Role of Ethylene Synthesis and Perception in the Acquisition of Abscission Competence
Lashbrook, C.C. **Grant 97-35100-4192**

University of Florida **Postdoctoral Fellowship**
Horticultural Sciences Department **$90,000**
Gainesville, FL 32611-0690 **2 Years**

Abscission is the process by which plants shed organs such as leaves, flowers and fruits. Organ detachment takes place within a layer of specialized cells called an abscission zone. Both developmental and environmental signals can activate plant organ abscission. Cotton, an important cash crop in the United States, is especially sensitive to environmental abscission signals. Significant shedding of cotton buds, flowers, young bolls and leaves can be triggered by variations in ambient temperature, water availability, nutritional status and insect pressure. Ethylene, a plant hormone, plays a critical role in promoting and coordinating abscission responses. Significant changes in ethylene synthesis and perception have been measured in detaching organs. The objective of this research is to elucidate the molecular mechanisms that regulate ethylene synthesis and perception in response to common abscission cues. Ethylene synthesis is dependent upon the enzymes ACC synthase and ACC oxidase. Enzymically produced ethylene is recognized by hormone receptors, called ETRs (Ethylene Response proteins), triggering a chain of events culminating in abscission. Genes encoding ACC synthase, ACC oxidase and ETR receptors will be cloned from ethylene-treated cotton abscission zones. The role of these genes in conferring abscission competence will be assessed in two experimental systems. Cotton leaves abscissing due to natural aging will serve as a model for developmentally-induced abscission. Cotton buds shed in response to water stress will serve as a model for environmentally-regulated abscission. An understanding of mechanisms conferring abscission competence in plants may ultimately suggest strategies to reduce premature abscission in agriculturally important crops.

9702703 Role of Ethylene Perception in Defense Responses to Pathogen Infection in Tomato
Lund, S.T. **Grant 97-35303-4786**

University of Florida **Postdoctoral Fellowship**
Department of Horticultural Sciences **$90,000**
Gainesville, FL 32611-0690 **2 Years**

Disease tolerance is defined as the ability of plants to produce a good crop even when they are infected by pathogens. Disease symptoms, characterized by widespread death of leaf and stem tissues, are reduced in tolerant plants even though pathogen spread is unaffected, thereby placing little selective pressure on pathogen populations. In contrast to disease tolerance, disease resistance entails the rapid activation of plant defense responses aimed at limiting pathogen spread and extinguishing the pathogen. Breeding

for disease resistance has been a major focus of disease control strategies, but the instability of resistance due to rapidly mutating pathogen races has restricted anticipated gains in yield. The potential for tolerance as a durable means of disease control has not received considerable attention in any species. A tomato mutant called Never ripe is unable to perceive the signal, ethylene, which is produced by the plant in response to a variety of environmental stresses such as pathogen infection. Preliminary experiments demonstrated that ethylene insensitivity in Never ripe plants conferred tolerance of infections by three unrelated pathogens. This finding indicates that ethylene-induced death of tissues in normal tomato plants is a deleterious agronomic trait. This research will determine the physiological role of ethylene perception in regulating disease development in tomato and will examine the potential for exploiting the Never ripe mutation as an economically desirable trait.

9702936 The Basement Membrane as a Barrier to Baculovirus Dissemination in the Host
Harrison, R.L. **Grant 97-35302-4325**

Iowa State University **Postdoctoral Fellowship**
Department of Entomology **$90,000**
Ames, IA 50011-3222 **2 Years**

Baculoviruses are a group of insect viruses that infect and kill many significant agricultural pests. Baculovirus-based pesticides are an attractive alternative to chemical pesticides since they do not pose the health and environmental risks associated with chemical residues. However, pests infected with baculoviruses continue to feed and cause crop damage for days or even weeks. As result, in many cases baculoviruses have failed to be commercially useful in the field. To improve their pesticidal efficacy, baculoviruses have been engineered with genes encoding a variety of toxins, hormones, or enzymes that paralyze pests or disrupt their development. I propose to investigate a novel, complementary strategy for improving baculovirus pesticidal efficacy which involves enhancing the capacity of baculoviruses to penetrate physical barriers to infection within the host. One of these barriers appears to be the basement membrane, an extracellular layer of protein which surrounds the tissues of all animals, including insects. I will engineer the baculovirus *Autographa californica* (alfalfa looper) nuclear polyhedrosis virus (AcNPV) with genes encoding enzymes that degrade the basement membrane. I will test the ability of this genetically modified AcNPV to circumvent the basement membrane barrier and establish a more extensive infection of the pest *Heliothis virescens* (tobacco budworm). I will then engineer AcNPV with genes for both a basement membrane-degrading enzyme and an insect-specific toxin, and I will measure the improvement in the pesticidal efficacy of this virus. The results of this research will augment the potency and commercial viability of baculoviruses as biological insect control agents.

9702988 Elucidation of the Cell Death Pathway in the Hypersensitive Response
Mach, J.M. **Grant 97-35303-4785**

University of Chicago **Postdoctoral Fellowship**
Department of Molecular Genetics and Cell Biology **$85,000**
Chicago, IL 60637 **2 Years**

When a plant is attacked by bacteria, viruses, or fungi, the plant cells can activate many different defenses, reinforcing their cell walls and secreting antibiotic compounds. The cells in the immediate vicinity of an infection also activate cell death, dying in order to protect the rest of the plant. My advisor, Dr. Jean Greenberg, has isolated accelerated cell death (acd) mutants, plants that activate cell death in the absence of infection. I plan to find genes required for the activation or execution of cell death by looking for mutations that change the cell death characteristics of the acd mutant plants. For example, a mutation that inactivates a gene which is absolutely required for the
process of cell death would prevent the acd plant cells from dying. I plan to characterize the effects of these mutations and eventually clone the gene responsible.

At the same time, I will clone the gene for one of the acd mutants, acd2. Previous work in Dr. Greenberg's lab has isolated a large block of DNA containing the acd2 locus. I will find the locus within the cloned DNA by introducing fragments of cloned DNA into acd2 mutant plants; any DNA fragment that can complement, or cure, the cell death characteristics of the acd2 mutant plants must contain the acd2 locus. I will also look for genes that are expressed in the dying cells by comparing the mRNA pools of dying and normal cells. Thus, I will characterize cell death in the accelerated cell death mutant acd2 both genetically and molecularly by looking for interacting genes and by cloning the acd2 gene.

9701918 Role of AvrPto-Pto Binding in Pto-mediated Disease Resistance
Bogdanove, A.J. **Grant 97-35303-4872**

Purdue University **Postdoctoral Fellowship**
Department of Agronomy **$90,000**
West Lafayette, IN 47907-1150 **2 Years**

The proposed research is directed toward understanding plant defense against pathogens using a model system. It seeks to determine the role of the avirulence gene product AvrPto of the bacterial speck pathogen, Pseudomonas syringae pv. tomato, in the activation of defense responses mediated by the tomato resistance gene, Pto. Recently, in a recombinant yeast system, AvrPto was discovered to interact directly with the product of Pto, a serine/threonine protein kinase. How does the interaction of these two proteins lead to various plant defense responses? Does AvrPto affect the enzymatic activity of Pto, and does AvrPto affect interactions of Pto with other signaling components? The proposed experiments address these questions directly. They include localization studies for the AvrPto-Pto complex in transgenic plants, a novel assay to detect AvrPto translocation into plant cells, use of Pto mutants with AvrPto in a binding assay and transient expression of these proteins in plants to test the relationship between binding and function, measurement of the effect of AvrPto on Pto enzymatic activity, and use of a modified yeast system to test the effect of AvrPto on the interactions of Pto with other proteins. In seeking to understand the role of AvrPto-Pto binding in activation of plant defense, the work proposed promises a significant contribution to the knowledge base required for effective, broad, and durable deployment of it-gene-mediated disease resistance through direct genetic manipulations

9701974 Molecular Markers for Resistance and Construction of a BAC Library in Strawberry
Haymes, K. **Grant 97-35300-4586**

USDA Agricultural Research Service **Postdoctoral Fellowship**
Fruit Laboratory **$90,000**
Beltsville, MD 20705 **2 Years**

The goal of this research project is to develop DNA markers for three resistance genes in the commercial strawberry that confer resistance against a fungal disease called *Phytophthora fragariae*. Previously, we utilized a technique called bulked segregant analysis to identify random amplified polymorphic DNA (RAPD) and amplified fragment length polymorphism (AFLP) markers to find linkage to *P. fragariae* resistance genes. The bulked DNAs represented subsets of three F1 populations that segregated monogenetically (1:1) for either resistance or susceptibility to *P. fragariae*. A genetic map was constructed and the markers linked to the resistance gene were shown to be linked. Based upon these initial results, we propose the following objectives: 1) to convert the genetic markers linked to the genes into highly specific markers, 2) to assess the strawberry germplasm for the conservation of the molecular markers to the genes, and 3) to construct a bacterial artificial chromosome library of the strawberry so that we may someday obtain the actual genes for resistance to this disease.

Strawberry breeding programs will benefit from the application of these molecular markers linked to resistance genes by providing an efficient means to screen and select plant material containing resistance genes, and by allowing marker-facilitated selection of these resistance genes. A long-term goal of this research is to reduce the amount of chemical fumigants used to grow strawberries. Genetic improvement of the strawberry by the ability to pyramid resistance genes will contribute to the productivity of the strawberry industry.

9701396 Ethylene-response and Senescence-related *Arabidopsis* Mutants
Larsen, P.B. **Grant 97-35304-4921**

University of Maryland, College Park **Postdoctoral Fellowship**
Department of Plant Biology **$90,000**
College Park, MD 20742-5815 **2 Years**

Ethylene is a simple gaseous hormone that plays numerous roles in plant growth and development, including fruit ripening and senescence. Significant progress has been made in understanding how a plant cell perceives ethylene and how this signal is transmitted to ultimately result in the initiation of complex physiological responses, yet large gaps in our knowledge exist. *Arabidopsis thaliana* (wall cress) has served as an excellent model organism for identification of genes that encode proteins involved in ethylene perception. These include several potential ethylene receptors and other intermediate components of the signal transduction pathway. These genes have been identified through the isolation of *Arabidopsis* mutants that have defects in ethylene perception as assessed by an ethylene-mediated phenomenon known as the seedling triple response. The specific goal of this proposal is to isolate additional components of the ethylene signal transduction pathway through the identification of *Arabidopsis* mutants that have alterations in other ethylene-mediated processes. Mutants that either have an increased sensitivity to ethylene (as assessed by root growth) or that have altered patterns of leaf senescence (a physiological process shown to be mediated by ethylene) will be identified. Ultimately, these mutants should allow for the isolation and characterization of presently unidentified genes that encode proteins that comprise the ethylene signaling pathway. Isolation of these genes should lead to a

more complete understanding of hormone perception in plants along with additional opportunities for controlling ethylene responses, an important issue in agriculture and more specifically, post-harvest technology.

9703922 Verification and refinement of QTL for carcass traits on swine chromosome 6
Miller, L.M. **Grant 97-35205-5079**

University of Minnesota, St. Paul **Postdoctoral Fellowship**
Department Veterinary PathoBiology **$90,000**
St. Paul, MN 55108-6010 **2 Years**

This project proposes to verify and refine the position of putative genes, called quantitative trait loci (QTL), responsible for carcass traits distinct from a disease causing gene (*ryr1*) on swine chromosome 6. It has long been recognized that numerous lean carcass characteristics are associated with the Porcine Stress Syndrome (PSS) causing allele at this locus. Because of this linkage, selection for leanness concomitantly increases the incidence of PSS which results in increased mortality and inferior meat quality. It is therefore important to better define the chromosomal region responsible for superior carcass qualities in order to improve these traits independently of the *ryr1* locus. A previous QTL scan of the Illinois reference family (Meishan X Yorkshire) identified a possible QTL for loin eye area positioned between markers adjacent to *ryr1*. Newly developed and existing markers will be genotyped on this family and included in a second analysis to refine the QTL position and effect. Chromosome 6 markers will then be genotyped on an additional resource population to evaluate their usefulness in identifying QTL in this population. This project should identify markers appropriate for use in marker assisted selection to improve this economically important trait in commercial swine herds.

9702442 Interferon-tau Expression and Action during Pregnancy
Ealy, A.D. **Grant 97-35203-4767**

University of Missouri, Columbia **Postdoctoral Fellowship**
Department of Animal Sciences **$90,000**
Columbia, MO 65211-5300 **2 Years**

The main goal of this work is to provide a better understanding of the actions of interferon-tau proteins. These proteins are secreted from the developing embryo of ruminant species, such as sheep and cattle, during early pregnancy and are responsible for signaling the presence of the embryo to the mother during early pregnancy, this event is required in order for pregnancy to be maintained in these species. Numerous genes encode for interferon-tau in sheep and cattle, but it remains unknown which of these genes encode for protein products that are primarily responsible for acting as pregnancy recognition signals. Through this work, the predominant variants of interferon-tau that are produced by the ovine embryo will be identified. In addition, recombinant proteins of these expressed gene variants will be produced in bacteria and will be used to identify those protein variants that are most potent at mimicking the events of early pregnancy when injected into the uterus of nonpregnant ewes. The final goal of this work is to begin to elucidate the means by which interferon-tau acts on the uterus to elicit pregnancy recognition signals, and, in particular, to identify signaling systems within the uterus that are responsive to interferon-tau. This knowledge will be very useful for increasing our basic understanding of early pregnancy in ruminants and, may lead to the development of schemes that can improve pregnancy rates in sheep and cattle.

9703082 Characterization of the bovine P2XA$_7$ Receptor in Cattle
Smith, R.A. **Grant 97-35204-4913**

University of Missouri, Columbia **Postdoctoral Award**
Department of Veterinary Pathobiology **$90,000**
Columbia, MO 65211-0000 **2 Years**

A bovine tuberculosis eradication program in the United States has substantially reduced the number of tuberculin reactive cattle since its implementation in 1917. However, the complete eradication of *Mycobacterium bovis* has not been possible because similar programs do not exist or are not as stringent in other American countries. *M. bovis* transmission from infected foreign cattle to U.S. herds exists and has been a problem for herds along the U.S.-Mexico border. In addition, the nature of *M. bovis* allows the transmission from humans and wild and exotic domestic animals to cattle. A general understanding of how mycobacterium, in particular *M. bovis*, is killed by the immune system is essential for determining the most effective routes for eliciting and immune response that will efficiently clear mycobacterium infection and can potentially be used in vaccine protocols. *M. bovis* resides inside of monocyte/macrophage cells of the animals they infect. ATP-induced cell death of monocytes is associated with the intracellular killing of the Calmette-Guerin strain of *M. bovine.* Additionally, P2X$_7$, an ATP-regulated receptor is involved in cell death of murine macrophages. In this study, the bovine homolog of the P2X$_7$ receptor will be cloned and both the bovine and murine receptors will be characterized. This information will be used to evaluate the role of this receptor in mycobacterial clearance from infected cells and determine further potential value in vaccine strategies.

9700900 Molecular Basis for Selenium Regulation of Glutathione Peroxidase mRNA Level
Weiss, S.L. **Grant 97-35200-4257**

University of Missouri, Columbia **Postdoctoral Fellowship**
Biochemistry/Nutritional Sciences **$90,000**
Columbia, MO 65211-0001 **2 Years**

Selenium is both essential and toxic. We hypothesize that cells can sense and respond to selenium status because of specific genes which direct the fate of selenium. Glutathione peroxidase (GPX) is a protein which contains selenium, and the messenger RNA (mRNA) for GPX is dramatically reduced in selenium deficiency, perhaps to ensure that selenium is used only for critical roles. Thus, we propose that GPX mRNA level is a parameter which directly indicates intracellular selenium status. For the present research project, specific mutations will be introduced into the DNA which encodes GPX and the gene constructs will then be transferred to mammalian cells in culture. Mutant GPX mRNA levels will be determined in selenium-deficient and selenium-adequate cells. These studies will identify the minimal DNA sequences required for selenium regulation of GPX mRNA. The minimal sequences should also be capable of conferring selenium responsiveness to mRNAs which are not normally affected by selenium. A second approach will focus on shifting the cellular selenium requirement for GPX mRNA level by altering the ability of cells to synthesize selenium-containing proteins. The most recent (1996) WHO/FAO/IAEA report suggests that humans require only 40 µg selenium per day, much less than a typical American consumes. This amount of selenium is needed for approximately two-thirds of maximal GPX activity in plasma. The present research project will further our understanding of selenium requirements at the intracellular level so that convenient parameters such as plasma GPX activity might be used with confidence to determine selenium requirements in humans.

9700974 A Seasonal Study of Diversity and Abundance of Nitrifying Bacterial Populations
Gsell, T.C. **Grant 97-35107-5064**

University of Montana **Postdoctoral Fellowship**
Division of Biological Sciences **$88,413**
Missoula, MT 59812-1002 **2 Years**

Nitrification is a subprocess of the nitrogen cycle whose critical steps are mediated by bacteria. Nitrification is particularly important in agro-economic systems because it facilitates mobilization of nitrogen added as fertilizer, affecting both uptake by plants and loss from the system. Nitrifying bacteria are notoriously difficult to study using standard culture-based methodologies. Molecular techniques have facilitated progress in the study of specific nitrifier populations, but emphasis on nitrification and nitrifiers in the context of the total bacterial community has been lacking. The objective of this study is to determine and compare the diversity and abundance of nitrifiers from disparate environments. This study will focus on the hypothesis that in areas of high ammonia-N abundance (e.g. in traditional agricultural management) a lower diversity of nitrifiers exists, with primarily ammonia-insensitive types being dominant. Conversely, in areas of low ammonia-N concentration, a greater diversity of ammonia-sensitive nitrifiers will prevail. This hypothesis will be tested through a comparative analysis of agricultural soils, prairie soil, forest soil, river water and sediments, an oligotrophic lake, a hyper-eutrophic lake, marine water and sediment, and estuarine waters and sediments. The main objective of this research is to determine whether the nitrifying community from agricultural sites is distinct from non-agricultural nitrifier profiles in a cross-season comparison. For each sample, ammonia-N concentrations will be determined. The relative abundance of ammonia-sensitive and -insensitive, nitrifier populations will be determined. Total bacterial community DNA purified directly from each sample will be analyzed using molecular techniques which will generate diversity indices for populations participating in nitrification across sites and through seasons.

9701313 Apocarotenoid Biosynthesis and Function in Plants
Schwartz, S.H. **Grant 97-35301-4427**

University of Nevada, Reno **Postdoctoral Fellowship**
Department of Biochemistry **$ 80,000**
Reno, NV 89557-0014 **2 Years**

Apocarotenoids are derived from the oxidative cleavage of carotenoids. These molecules are widely distributed in nature and serve important biological functions in diverse organisms. Vitamin A, for example, is necessary for development and vision in animals. In plants, abscisic acid (ABA) serves a role in seed development and adaptation to a variety of stresses. Many additional apocarotenoids have been identified in plants, but their functions remain speculative. The biosynthesis of apocarotenoids is catalyzed by enzymes that oxidatively cleave carotenoids. There is evidence for this type of enzyme in organisms from all five kingdoms, but little progress has been made in their characterization. Recently, the gene encoding a cleavage enzyme for ABA biosynthesis has been cloned. The identification and characterization of this gene has provided the basis for identifying additional carotenoid cleavage enzymes. The primary goals of this project are to elucidate the function of apocarotenoids in plants and to clone the genes necessary for their synthesis.

9701436 Cloning of a Recessive Bacterial Disease Resistance Gene from Rice
Blair, M.W. **Grant 97-35300-5101**

Cornell University **Postdoctoral Fellowship**
Department of Plant Breeding **$90,000**
Ithaca, NY 14853-1902 **2 Years**

Plant pathogens cause disease by producing virulence factors that manipulate host metabolism to the plant's detriment and the pathogen's benefit. These virulence factors may increase disease susceptibility by tricking plant proteins into becoming unwitting collaborators of the pathogen. However, the molecular mechanisms of disease susceptibility are not as well understood as the recognition and defense response systems that can be activated by plants when they are attacked. This research will determine whether resistance can result from recessive mutations that block disease susceptibility genes in plants. Recessively-inherited resistance is a common phenomenon for diseases caused by fungal, bacterial and especially viral plant pathogens. In this project, a recessive resistance gene from rice, xa-5, that provides vertical, race-specific resistance to the bacterial leaf blight pathogen, *Xanthomonas oryzae pv. oryzae*, will be isolated by a strategy of map-based cloning and complementation testing. Positional cloning has a successful track record in rice because of its small genome size and complete "toolbox" for genetic analysis. The cloning of the recessive resistance and dominant susceptibility alleles of xa-5 may uncover a unique class of genes and provide molecular evidence for how these genes function. The structure of the cloned gene may help to explain how plant-pathogenic xanthomonad bacteria are able to attack so many of the vegetable, fruit, cereal and fiber crops important to U.S. agriculture. This knowledge will have significant practical implications for long-lasting management of resistance and for engineering new disease resistance strategies by interfering with the underlying processes of plant pathogenesis.

9700661 Vitamin A-Dependent Regulation and Function of *Hox* Genes in Development
Packer, A.I. **Grant 97-35200-4291**

Columbia University College of Physicians and Surgeons **Postdoctoral Fellowship**
Department of Genetics and Development **$89,163**
New York, NY 10032 **2 Years**

Vitamin A is of fundamental importance in maintaining the normal functions of cells and tissues in fetal development and in adult life. One recent finding suggests that a slightly elevated intake of vitamin A during pregnancy is associated with an increased risk of birth defects; others suggest that vitamin A supplementation may be a promising treatment for premature infants prone to respiratory distress and infection. A better understanding of the roles and mechanisms of action of the vitamin A derivatives--the retinoids--is needed in order to determine appropriate levels of dietary vitamin A during pregnancy and for the identification of other ways in which nutritional status affects human health. Basic studies in experimental models such as the mouse have demonstrated that the retinoids function by regulating the expression of a variety of genes during fetal development. I have proposed a series of experiments to study the retinoid-dependent regulation and potential function of a *Hox* gene, *Hoxa*-4, in mice. *Hox* genes are critically important for normal embryonic development in many organisms, including mice and humans, and a growing body of evidence suggests that altered vitamin A metabolism affects development, at least in part, by altering *Hox* gene expression. Our preliminary observations indicate that *Hoxa*-4 is likely to be regulated directly by retinoic acid (a vitamin A derivative), and its expression in tissues where retinoids are known to be important—the hindbrain, lung, and kidney--makes it an excellent model in which to study how suboptimal and/or elevated levels of retinoids affect development. The study will examine the manner and timing of vitamin A-dependent activation of *Hoxa*-4, and will explore the possibility that vitamin A affects fetal lung and kidney development by regulating the expression of *Hoxa*-4 and other related *Hox* genes.

9701369 Occurrence and Synthesis of the Auxin Conjugates of *Arabidopsis thaliana*
Barratt, N.M. **Grant 97-35304-5107**

Case Western Reserve University **Postdoctoral Fellowship**
Department of Biology **$81,000**
Cleveland, OH 44106-7080 **2 Years**

The plant hormone auxin plays a major role in control of plant growth and development, regulating such processes as elongation and directional growth, development of fruit and vascular tissue, and senescence. Agronomic applications of auxins include use in fruit production and as herbicides. The major endogenous auxin in plants is indole-3-acetic acid (IAA). Precise modulation of IAA levels is key to normal plant growth. In most plants, the bulk of IAA exists not as free, active, hormone, but chemically linked or conjugated to other molecules such as amino acids or sugars. IAA conjugates may serve as forms of the hormone for storage or transport, protection from degradation, or inactivation. The abundance and universality of conjugates suggests the compounds are important in regulation of endogenous hormone levels. The diversity of endogenous and synthetic auxin conjugates suggests individual conjugates may play roles specific to a developmental stage or stimulus. Despite this, little is known of the identities or actions of auxin conjugates in any species. This project will first identify the full complement of

endogenous conjugates in *Arabidopsis thaliana* (a wild mustard). Second, conjugate formation will be characterized in response to environmental stimuli such as light intensity and drought stress, and in response to other plant hormones with which auxin interacts. The model dicot, A*rabidopsis*, lends itself well to molecular and genetic studies. An understanding of the identities and occurrence of endogenous conjugates in this species will facilitate study of genes and enzymes involved in auxin metabolism.

9702568 *Salmonella typhimurium* Genes Required for Systemic Infection of Cattle
Tsolis, R.M. **Grant 97-35201-4505**

Texas A&M University **Postdoctoral Fellowship**
Department of Veterinary Pathobiology **$90,000**
College Station, TX 77843-4467 **2 Years**

Salmonellosis is the most frequent food-borne illness in the U.S. and is usually contracted by consumption of meat and dairy products from infected livestock. Little is known about genes allowing *Salmonella typhimurium* to cause systemic infection in cattle, an important meat source in the U.S. Since systemic infection can lead to a chronic carrier state, information about the mechanisms used by *S. typhimurium* to establish systemic infection is relevant to development of strategies to eliminate this pathogen from cattle. The goals of this project are the identification and characterization of bacterial genes which enable *S. typhimurium* to cause systemic infection in cattle. The role that these genes play during infection will be examined by determining the ability of attenuated bacterial mutants to spread to different organs in cattle. Finally, by determining whether the same set of virulence genes identified in cattle is also required for infection of the mouse, we will determine whether any of the genes identified in this study are host-specific adaptations to causing disease in cattle. The results of this research will help to develop strategies for reducing the number of carrier animals from cattle herds as well as for the detection of *Salmonella* in meat and dairy products, thereby increasing food safety.

9702935 Alkalinization and Ion Transport by Larval Mosquito Midgut
Clark, T.M. **Grant 97-35302-4919**

Washington State University **Postdoctoral Fellowship**
Department of Zoology **$84,578**
Pullman, WA 99164 **2 Years**

Mosquitoes and blackflies transmit a wide variety of viral, bacterial, protozoan, and filarial diseases of animals and humans. In addition to disease transmission, these biting flies cause loss of livestock production due to biting distress, and can at times become so numerous that livestock die from blood loss, immune shock, or suffocation. Less severe effects to cattle include an immediate reduction in milk yield that may last 1.5 months following attack, reduced gain in liveweight, reduced fertility, a higher percentage of dry cows, and loss or trampling of calves. These effects of biting flies on livestock production can be avoided or ameliorated by preventing mass outbreaks of mosquitoes and blackflies. Development of resistance to insecticides has led vector control agents toward use of more specific biological control materials, including microbial insecticides, parasites, and pathogens aimed at the larval stages. Efficacity of biological control agents is determined by the alkalinity of the insect gut. Larval mosquitoes and blackflies have very alkaline midgut contents (pH 10). This high pH is necessary for infectivity of some biological control agents but prevents activity of others. Agents that are presently ineffectual in mosquito control due to destruction of the agent by the high pH within the gut could become viable control agents if normal gut function is compromised, allowing infection to occur. The purpose of this research is to identify the mechanisms used by the insect to alkalinize its midgut contents, information expected to improve the efficacity and cost-effectiveness of biological control agents.

9700770 Coupling Agroecosystem Geographic Information Systems with Neural Network Models
Hart, G.L. **Grant 97-35101-4373**

University of Wisconsin, Madison **Postdoctoral Fellowship**
Department of Soil Science **$81,330**
Madison, WI 53706-1299 **2 Years**

Artificial neural networks (ANN) have been used in a wide variety of applications including neuroscience , electronics, robotics, process control, image and voice recognition, and financial analysis. Artificial neural networks have also been utilized as tools to enhance conventional statistical techniques. Geographic information systems (GIS) such as ARC/INFO are utilized extensively in digitizing, managing, and displaying spatial data on landscape scales. Because of the complex, multivariate factors which interact to affect agroecosystems and the extensive landscapes over which these systems are managed, it has become a common theme recently to couple GIS with computer simulations to address certain production, economic, and environmental issues. However, no one has designed or employed a technique to analyze these data to address questions concerning agricultural productivity, sustainability or resource management issues at the scale of agroecosystems. Directly extrapolating experimental plot data to landscape scale has serious limitations. A primary reason for this limitation is that cause and effect relationships can

not be easily deduced from small-scale experiments (research plots) conducted on segments of agroecosystems, making interpretation and application of experimental results difficult or impossible. This project will investigate the possibility of using ANN models to assess a range of interrelated components of agroecosystems. Coupling a GIS database with a trained neural network model could advance our understanding of interactions and aid in management of complex agricultural systems.

9701274 Epigenetic Mechanisms and Changes in Gene Expression Associated with Flowering
van Nocker, S. **Grant 97-35304-5108**

University of Wisconsin, Madison
Department of Biochemistry
Madison, WI 53706

Postdoctoral Fellowship
$90,000
2 Years

The transition from a vegetative to reproductive state (flowering) represents a major developmental event in flowering plants, and is an essential component of agricultural production. Many plants exhibit accelerated floral initiation in response to an extended cold treatment. This response, termed vernalization, helps to coordinate flowering and subsequent seed production with favorable environmental conditions. I propose to identify the molecular mechanism(s) associated specifically with vernalization, using the reference plant *Arabidopsis thaliana* as a model system. Because the process of vernalization is likely associated wich changes in gene expression, this goal will be approached by identifying genes that are differentially expressed in vernalized vs. non-vernalized plants through differential gene cloning techniques.

Characteristics of vernalization, including the requirement for mitosis during the cold treatment and the mitotic but not meiotic transmission of the vernalized state, strongly implicate the involvement of epigenetic phenomena. Recent studies in *Arabidopsis* demonstrate the involvement of genomic DNA methylation in a myriad of developmental events, including the transition to flowering. As a complementary approach to identifying vernalization responsive genes, I will attempt to identify specific changes in genomic DNA methylation between vernalized and non-vernalized plants, which may be associated with changes in gene expression. This will be accomplished by applying an established technique used for the identification of genotype-specific polymorphic marker sequences to the identification and isolation of methylation-dependent, polymorphic sequences.

An understanding of the mechanisms responsible for vernalization-associated floral initiation, in addition to obvious agricultural benefits, will contribute greatly to our understanding of plant development in general.

NEW INVESTIGATOR AWARDS

New Investigator Awards are intended to enhance the ability of investigators beginning their research careers in obtaining competitive grants from the NRI. New Investigator Awards are reviewed in the program area most appropriate for the type of research proposed; therefore, these nontechnical summaries also appear under the respective program areas.

9702584 Mechanism and Determinants of Sperm Precedence in *Heliothis virescens*
LaMunyon, C.W. **Grant 97-35302-4869**

University of Arizona
Department of Molecular and Cellular Biology
Tucson, AZ 85721-0106

New Investigator Award
$100,000
2 Years

This study seeks to provide information useful in developing more effective methods for controlling the tobacco budworm moth, *Heliothis virescens*, a major pest of cotton, soybeans and other crops. Because of its increasing resistance to pesticides, alternative methods are needed to control the budworm. One method, the sterile male technique, involves rearing and release of large numbers of sterilized males, which pass non-functional sperm and thereby sterilize females. This method has not been effective for the budworm because the females mate with more than one male; thus a fertile mating may reverse the effects of a sterile mating. Previous studies have shown that multiple-mated females lay eggs fertilized by only one of their mates. In related species, males that gain successful paternity exhibit certain traits, such as large body size. This project aims to identify such male traits in the tobacco budworm moth. Female moths will each be mated to two males and offspring paternity determined biochemically. Male traits, including age, mass, symmetry, ejaculate size and sperm content will be assessed as potential determinants of paternity. To investigate the mechanism by which certain males gain paternity, the pattern of sperm storage within the various parts of the complex female reproductive tract will be studied as a function of the male traits that affect paternity. The results will improve our knowledge of the reproductive biology of this important pest and may provide information to allow the breeding of males with highly competitive ejaculates for sterile male control efforts.

9701278 Genetic Analysis of *Arabidopsis* Receptor-like Kinases Using Insertional Alleles
Tax, F.E. **Grant 97-35304-4708**

University of Arizona
Department of Molecular and Cellular Biology
Tucson, AZ 85721

New Investigator Award
$90, 000
2 Years

In multicellular organisms, cells communicate information to other cells during development. These signals can determine the specific function of cells. While there has been experimental evidence for intercellular signaling in plants for more than 20 years, the specific molecular mechanisms involved have not been well characterized. In animals, receptor protein kinases play key roles during development by responding to extracellular growth factors and regulating intracellular transduction pathways. A large number of plant proteins resembling animal receptor kinases have been found, but since no ligands have yet been conclusively identified, these have been called receptor-like kinases (RLKs). More than twenty different RLKs have been found in various sequencing projects in *Arabidopsis* (mouse-eared cress), but the specific functions of only two or three are known from the analysis of mutants. One way to identify the role of a gene is to identify a mutation in that gene, To determine the function of some of these additional RLKs in *Arabidopsis*, a reverse genetics method has been used to identify insertions in four different RLKs. The goal of the proposed work is to analyze these mutations and characterize the phenotypic consequences of these insertions.

9702140 Iron Metabolism in Lepidopterans
Winzerling, J.J. **Grant 97-35302-4458**

University of Arizona
Department of Nutritional Sciences
Tucson, AZ 85721-0038

New Investigator Award
$200,000
2 Years

Iron is a required nutrient for all living creatures. A good deal is known about plant and animal iron nutrition, and these two organisms use iron differently. In contrast, there is little information about insect iron metabolism. We are studying how insects take up and utilize iron. Insect iron metabolism appears similar to that of man, but with some subtle and important differences. Two proteins that are directly involved in iron metabolism in mammals are the iron regulatory protein (IRP1) and the transferrin receptor. These two proteins are present in insects, but do not function in plants. We will characterize the IRP1 and the transferrin receptor in caterpillars. We can then study when these proteins are made, how their synthesis is controlled and how they function in this insect model. Such information could increase our understanding of how iron and other transition metal ions affect insects. In addition, knowledge of differences in iron metabolism among various organisms could be used to suggest compounds or strategies for insect control that do not affect the iron metabolism of humans or plants. We selected caterpillars as a working model because insects from this order are well studied pests that cost millions of dollars each year by their destruction of crops, forests and fabrics.

9701779 Positional Cloning of *Triticum monococcum* Vernalization Genes
Dubcovsky, J. **Grant 97-35300-4379**

University of California, Davis
Department of Agronomy and Range Science
Davis, CA 95616-8515

New Investigator Award
$250,000
3 Years

The adaptability of bread wheat to a large range of environments is partially due to the exploitation of genetic differences in sensitivity to vernalization. The objective of this project is to develop the molecular tools required for the positional cloning of these important genes. Cloning
of wheat vernalization genes will not only provide a new understanding of the biochemical nature and genetic regulation of the vernalization response in winter cereals but also provide a new tool for the manipulation of the vernalization response in wheat.

The first objective of this proposal is to develop high-resolution genetic maps of vernalization genes in wheat. Two crosses between spring and winter diploid wheats will be used to generate large mapping populations. Available molecular markers for the targeted chromosome regions will be mapped simultaneously with the vernalization response. High throughput molecular marker technologies and regional targeting strategies will be used to develop closely linked markers encompassing the vernalization genes.

The second objective of this proposal is to clone the complete genome of diploid wheat using Bacterial Artificial Chromosomes (BACs). The BAC library will have one hundred BAC clones with inserts of 150 to 200 kilobases and will be a long-term tool for positional cloning of different
cereal genes.

The most closely linked markers flanking each vernalization gene will be used to screen the BAC library. The ends of the selected BAC clones will be mapped in the high-resolution genetic maps to confirm the presence of the genes within the selected BAC clones.

9701250 The Positive Effect of Introns on Plant Gene Expression
Rose, A.B. **Grant 97-35301-4392**

University of California, Davis
Section of Molecular and Cellular Biology
Davis, CA 95616-8535

New Investigator Award
$110,000
2 Years

The information contained in most plant genes is interrupted by non-coding sequences known as introns. Introns are deleted after the gene has been transcribed into mRNA but before the mRNA is translated into protein. Introns are not simply a kind of packaging material that must be removed before the information in a gene can be read. In many examples, the amount of protein derived from a gene is greatly increased by the presence of an intron. Currently, the means by which introns enhance expression are not known.

The goal of this project is to determine the mechanistic basis for the positive effect of introns on the expression of plant genes. Experiments to achieve this goal will be performed with a well characterized and versatile test system consisting of a gene that has been modified to facilitate the quantification of gene expression, and one of that gene's natural introns which can be easily isolated and experimentally manipulated. The main question to be answered is whether or not there are specific DNA elements within an intron that are required to increase expression, or alternatively, whether the process of intron removal is necessary and sufficient for this enhancement.

This research will increase our understanding of a very important but poorly understood fundamental aspect of plant gene expression. A deeper understanding of the factors needed for abundant gene expression could have enormous practical benefit because there are many scientific and commercial applications in which a high level of protein synthesis is desirable.

9700718 Production of Phenolic Antioxidants in Response to Environmental Stress
Grace, S.C. **Grant 97-35100-4390**

University of Colorado
Department of Environmental, Population and Organismic Biology
Boulder, CO 80309-0334

New Investigator Award
$92,000
2 Years

Many types of environmental stress cause an increase in the production of phenolic secondary compounds in plants. One such compound is chlorogenic acid, a major product of the plant phenylpropanoid pathway. Despite its natural abundance, the biochemical function of chlorogenic acid in plants is unknown. Recent pharmacological studies have revealed that chlorogenic acid and related plant diphenols possess powerful hydrogen donating (antioxidant) properties against a variety of oxidizing and potentially harmful free radicals. Yet there has been little investigation of whether these compounds function as antioxidants within plants themselves. This question has been the subject of recent research into the mechanisms of stress tolerance in the evergreen shrub *Mahonia repens*. Leaves of this species produce large amounts of chlorogenic acid when exposed to the

combined environmental stresses of high light intensity and low temperature, whereas plants growing under deeply shaded conditions maintain low and nearly constant levels of chlorogenic acid throughout the year. More importantly, the ability of *Mahonia* leaf extracts to neutralize a range of oxidizing free radicals correlated directly with chlorogenic acid concentration, supporting an antioxidant role for this metabolite. The major aim of the proposed research is to extend these preliminary findings in a more thorough investigation of the seasonal changes in leaf chlorogenic acid concentration in relation to active oxygen scavenging activity in natural populations of *Mahonia repens*. Such a comprehensive analysis will greatly improve our understanding of the role and action of phenolic compounds in biochemical adaptation to environmental stress.

9702219 Ambrosia Beetle-plant Interactions: Influence of the Ambrosia Fungus Strain
Daehler, C.C. **Grant 97-35302-4262**

University of Hawaii, Manoa
Department of Botany
Honolulu, HI 96822

New Investigator/Strengthening Award
$180,000
3 Years

Ambrosia beetles bore into the wood of many economically important trees, inoculating the wood with an ambrosia fungus that they carry with them in a small pouch. The ambrosia fungus then grows within the bored tunnel, providing an essential food source for the beetle. In some cases, this fungus is pathogenic to the tree. This study aims to understand how genetic variation in the ambrosia fungus carried by an ambrosia beetle (the black twig borer) can influence both the severity of damage in attacked trees and the reproductive success of the beetle. Introduced to Hawaii in the 1960s, the black twig borer can cause severe damage to koa (*Acacia koa*), a fast-growing endemic tree that is prized for making high-value wood products. Previously established plots of some 3,000 koa saplings from 20 different families will be used to test for genetic variation in black twig borer resistance and variation in koa response to inoculation by different ambrosia fungus strains. Survivorship and growth of black twig borers carrying different ambrosia fungus strains will also be compared in the plots. Koa is a promising crop for planting in Hawaii's extensive abandoned sugar cane fields, and an understanding of the black twig borer-ambrosia fungus-koa interaction is needed to ensure continued successful growth of the koa wood industry in Hawaii. At the same time, this model system is expected to provide insights into how variation in an ambrosia fungus can interact with plant genetic variation to influence ambrosia beetle damage in other economically important trees.

9701723 Fine-Mapping a Crown Rust Resistance Gene Cluster in Diploid Oat
Holland, J.B. **Grant 97-35300-4865**

Iowa State University
Department of Agronomy
Ames, IA 50011-1010

New Investigator Award
$115,000
3 Years

Crown rust disease is the most damaging disease of oats in the U.S., causing significant losses in grain yield and quality every year. Genetic resistance to crown rust is the most economical and environmentally sound method of protection against the disease. The primary sources of genes for resistance to crown rust are the wild relative species of oats. We have identified a cluster of crown rust resistance genes all located in the same chromosomal region of a wild oat species, *Avena strigosa*. We propose to genetically "dissect" this complex group of genes using classical genetic techniques of crossing lines possessing different portions of this cluster together and examining their progeny for lines that contain only single resistance genes. This will allow us to unequivocally identify the individual genes that make up this cluster. We will combine these classical genetic approaches with modern molecular genetic techniques to develop a detailed understanding of these resistance genes. First, we propose to complete a genetic map of the entire genome of this species using DNA markers. In addition, we propose to identify numerous DNA markers within and surrounding the chromosomal region of this resistance gene cluster. The results of this research should provide information and materials (such as genetic stocks and DNA markers) that can be used by oat breeders to introduce and track these resistance genes from the wild species into cultivated oats, and lead to progress toward cloning of these resistance genes.

9700879 Translational Control of Gene Expression in Desiccation Tolerant Vegetative Plant Tissue
Wood, A.J. **Grant 97-35100-4476**

Southern Illinois University
Department of Plant Biology
Carbondale, IL 62901-6509

New Investigator Award
$105,000
2 Years

The vast majority of higher plants, including most important food crops, are susceptible to drought and incapable of withstanding desiccation. In order to gain a full understanding of stress-inducible processes in plants, it is often beneficial to develop simple model plants for study. Model plants that exhibit stress tolerant traits are useful tools in elucidating the molecular processes involved in tolerance and may provide unique genetic material that can impact breeding programs for improved crop stress management.

Tortula ruralis is a desiccation-tolerant bryophyte and has the potential to become an important model system for the study of posttranscriptional gene control in response to severe water deficit. In response to rehydration, desiccated *T. ruralis* produces a set of peptides unique to the rehydrative state utilizing a desiccation-stable mRNA pool. The changes in gene expression *in vivo* due to drying and rehydration are primarily mediated at the translational level; translational control mechanisms provide a sensitive and flexible response to environmental stresses. These data suggest that one mechanism for the observed mRNA stability and posttranscriptional gene control is the interaction of a *trans*-protein factor with specific mRNAs. The RNA gel mobility shift assay will be used to assess this possibility. Our proposed research will further characterize the unique posttranscriptional gene expression of *T. ruralis* by identifying and characterizing the RNA-binding protein(s) and investigating the nature of the mRNA-protein interaction.

9701416 Molecular and Developmental Analysis of Shoot Growth of *A. thaliana*
Pickett, F.B. **Grant 97-35304-4658**

Loyola University of Chicago **New Investigator Award/Strengthening Award**
Department of Biology **$90,000**
Chicago, IL 60626 **2 Years**

The genetic regulation of the development of plant embryos residing within seeds is largely unknown. By identifying mutants that disrupt normal embryo formation in predictable ways, we have identified genes that promote normal embryogenesis when present in their wild-type, non-mutant form. The identification of the proteins encoded by these genes will provide insight into the molecular mechanisms that guide cells in the embryo from a naive state, to a state in which the cells can play appropriate roles in the formation of leaves, stems and flowers. We will identify novel embryonic genes by exposing plants to mutagenic chemical and physical agents, and by screening in their offspring for the physical manifestations of these gene mutations. In addition to our mutant screens, we have begun to produce a fate map of the embryo of *Arabidopsis*, a cruciferous plant related to broccoli, cauliflower and canola. The fate map will provide the time and location during embryonic development when cells encounter regulatory cues that cause them to participate in the formation of the seedling leaves (cotyledons) and the meristem. The meristem acts as an enduring embryo, producing new organs throughout plant development. All of the visible structures of plants, including stems, leaves and flowers, develop when naive cells in the meristem receive regulatory cues. Thus our fate mapping and genetic analysis comprise a combined approach to first characterize developmental programs in the embryo and then analyze the molecular mechanisms that organize and direct these developmental programs.

9702528 Mode of Action of *Nosema apis*, a Microsporadian Pathogen of Honey Bees
Huang, Z.Y. **Grant 97-35302-4784**

University of Illinois, Urbana-Champaign **New Investigator Award**
Department of Entomology **$100,000**
Urbana, IL 61801 **2 Years**

Nosema apis is a cosmopolitan parasite of honey bees and causes significant negative impact on the beekeeping industry. Because of the central role honey bees play in pollination, this disease poses a serious threat to US agriculture. *Nosema* disease causes reduced life span in workers, reduced honey production, decreased winter survival, slower increase in colony size in the spring, and higher queen loss. The main changes of *Nosema* infected workers are earlier regression of hypopharyngeal glands (the glands that produce queen and larval food), and earlier onset of foraging. The mechanism through which *Nosema* causes these physiological and behavioral changes in bees is not known, but most likely it is related to a hormone that is normally produced in workers. Juvenile hormone regulates age-related physiological and behavioral changes in workers. This study attempts to examine whether *Nosema* produces juvenile hormone directly, or increases the host hormone concentration by either increased production or decreased degradation, or increases the sensitivity of host to their endogenous hormones.

This research will provide fundamental knowledge for the mechanism of honey bee endocrine and behavioral changes caused by *Nosema*. This knowledge would be a first step toward understanding the physiological and biochemical processes in *Nosema*. Such understanding would eventually be useful for designing highly specific pesticides for the control of *Nosema*.

9703996 Identification and evaluation of the acid meat (RN) gene in swine
Sunden, S.L.F. **Grant 97-35205-5078**

University of Illinois, Urbana **New Investigator Award**
Department of Animal Sciences **$290,000**
Urbana, IL 61801-3838 **3 Years**

Meat quality is an issue of increasing importance to animal agriculture and to the swine industry in particular. A recent US industry survey has shown that meat quality defects are a source of major economic loss to the swine industry. One quality issue of major concern in the US is the so-called "acid meat condition". This condition, as the name implies, results from a low ultimate

pH in the muscle post mortem. Compared to normal pork, acid meat is paler and has lower water holding capacity, which results in increased cooking loss and a reduction in processing yields. The net result is a negative impact on the financial return to the meat processor. On the other hand, acid meat has been shown to be more tender and the condition may be associated with enhanced growth and carcass characteristics. Thus, there is a potential advantage that may be of economic significance in certain situations. The goals of this project are to utilize a constellation of expertise and resources to identify the gene that causes the RN phenotype and characterize its effects on meat quality and production traits.

9703657 Regulation of Pituitary Development by the P-Lim Transcription Factor
Rhodes, S.J. **Grant 97-35206-5084**

Indiana University-Purdue University at Indianapolis **New Investigator Award**
Department of Biology **$120,000**
Indianapolis, IN 46202-5132 **2 Years**

The anterior pituitary gland contains specialized cells secreting hormones that regulate growth, lactation, reproductive development and status, thyroid physiology, and the stress response. During development, tissue-and cell-specific gene regulatory proteins coordinate the commitment and differentiation of the hormone-releasing cells. P-Lim is a pituitary-specific transcription factor essential for pituitary organogenesis: animals with mutated P-Lim genes do not develop anterior pituitary glands and die shortly after birth. The aim of this research is to characterize the mechanism of action of this critical protein in the pig. We will clone, sequence and characterize complementary DNA clones encoding pig P-Lim. To understand the transcriptional activity of P-Lim, the mechanism of pig pituitary target gene activation by P-Lim will be investigated. Further, to better understand hypothalamic and other signaling pathways that may regulate P-Lim function, modification of the pig P-Lim protein will be studied and the effects of such modification on P-Lim function determined. These studies will increase our understanding of essential developmental control mechanisms governing the central endocrine organ that coordinates growth, reproductive function and homeostasis in all animals of agricultural importance, including aquaculture species. This work will therefore guide future genetic and treatment protocols aimed at improving animal growth and fitness and will enable increased agricultural productivity.

9703930 Regulation of Leptin Gene Expression and Bioactivity in the Pig
Houseknecht, K.L. **Grant 97-35206-5093**

Purdue University **New Investigator Award**
Department of Animal Sciences **$110,000**
West Lafayette, IN 47907-1151 **2 Years**

Improving the productive efficiency of food animals requires understanding of the integrated biological processes involved in the regulation of adipose tissue metabolism, lean protein accretion and whole-body energy metabolism. Such processes are regulated by myriad hormones and growth factors which act to coordinate tissue nutrient utilization and food intake. The discovery of leptin, an adipostatin which senses and regulates body energy stores in rodents and humans, opens a new chapter in the understanding of energy metabolism. Circulating leptin levels in rodents and humans not only reflect body fat mass and nutritional status, but a hallmark of obesity is hyperleptinemia and leptin resistance. Data suggest that leptin may play a role in the development of peripheral insulin resistance associated with obesity. Leptin is also important in signaling insufficiency of adipose tissue stores during fasting or disease states. Our hypothesis is that leptin plays a key role in the regulation of feed intake and energy metabolism in the pig, and that regulation of leptin action may be important in optimizing animal growth performance and well-being. The first objective examines the role of fatty acids in regulating leptin expression *in vivo*. This includes quantifying adipocyte leptin expression in pigs fed isonitrogenous diets which vary in fat content (0-10%) and fatty acid profile (14:1/16: vs 18:2). The second objective involves identification of proteins in porcine serum which specifically bind leptin. The proportion of leptin in the free and bound state will be determined in fed and fasted, lean and obese pigs. Leptin binding proteins most likely play an important role in the regulation of leptin bioactivity and clearance rate.

9702742 Aggressiveness and Pathogenicity Determinants in Anthracnose Stalk Rot of Corn
Vaillancourt, L.J. **Grant 97-35303-4968**

University of Kentucky **New Investigator Award**
Department of Plant Pathology **$100,000**
Lexington, KY 40502-0091 **2 Years**

Fungal stalk rots are a major disease problem of corn. The anthracnose fungus, *Colletotrichum graminicola*, is one of the most common of these stalk rot fungi. The goal of this project is to identify genes from this fungus that are important in its ability to colonize and rot corn pith. If such genes can be identified and their functions determined, this information can be used to design controls for stalk rot disease in the future. The first step will be to develop and characterize a laboratory bioassay involving detached stem segments from mature corn plants. This will minimize the variability in disease severity caused by environment,

and allow us to concentrate on the variability determined by fungal genes. The next step will be to use the bioassay to screen a large number of isolates of *C. graminicola* for variation in pathogenicity and aggressiveness. Matings and genetic segregation analysis will be conducted among the most and least aggressive fungal isolates to determine the numbers and types of genes involved in pathogenicity and aggressiveness to corn pith. Finally, mutagenesis will be performed using selected fungal isolates, and the mutants will be screened for those with decreased pathogenicity and aggressiveness in the bioassay. These mutants can eventually be used to clone and characterize individual genes important for expression of the stalk rot syndrome.

9702121 Dimensional Stability and Durability of Oriented Strand Board
Wu, Q. **Grant 97-35103-5055**

Louisiana State University Agricultural Center **New Investigator Award**
School of Forestry, Wildlife and Fisheries **$49,000**
Baton Rouge, LA 70803 **2 Years**

Oriented strand board (OSB) is a hygroscopic product which is dimensionally unstable as moisture content changes. The dimensional change is often accompanied with permanent strength loss and sometimes product failure when exposed to high humidity conditions. The purpose of this work is to quantify the effect of the processing variables on the swelling behavior of OSB and to assess the extent of associated strength/stiffness loss. Single-layer and cross-laminated three-layer OSB panels were manufactured in the laboratory under various combinations of flake orientation, density, resin content, and, for the three-layer boards, face-to-core weight ratios. Tests will be conducted to determine flake alignment distribution, vertical density gradient, linear expansion (LE), thickness swelling (TS), bending stiffness and strength, and stress-wave modulus. Effects of the processing variables on the swelling and strength retention properties of the OSB will be examined and quantified. Using the data from the single-layer panels, a mathematical model will be developed to predict LE and TS of the three-layer, cross-laminated panels of different constructions. Through model analysis, importance of the various factors' significance in controlling the swelling behavior of the OSB will be investigated. It is expected that a successful completion of the project will lead to a fundamental understanding of the controlling mechanisms of the swelling behavior in OSB. This will allow OSB manufacturers to adjust the manufacturing process to minimize their effects.

9703022 Survival and Virulence of Enterohemorrhagic *Escherichia coli* (EHEC) as Affected by pH and Water Activity
Meng, J. **Grant 97-35201-4904**

University of Maryland **New Investigator Award**
Department of Nutrition and Food Science **$87,000**
College Park, MD 20742 **2 Years**

Enterohemorrhagic *Escherichia coli* (EHEC) have caused a series of foodborne outbreaks of bloody diarrhea as well as serious complications, including hemolytic uremic syndrome (HUS).
While research efforts have been focused on *E. coli* 0157:H7, it is becoming more evident that other serotypes of EHEC can also be associated with human diseases. An increasing number of non-0157 EHEC have been isolated from humans suffering from HUS and diarrhea. A variety of foods have been implicated in *E. col i* 0157:H7 outbreaks, particularly foods of bovine origin. Certain foods such as apple cider and dry-cured salami that were considered safe and ready to eat, and are generally not heated before consumption have been identified as transmitting vehicle in *E. coli* 0157:H7 outbreaks. Unlike 0157:H7, most of non-0157 EHEC serotypes have been isolated from sporadic cases, hence, the significance of food as vehicle for transmitting non-0157 EHEC is not clear. It has been shown that bacterial regulatory responses to environmental conditions are tied to virulence gene expression and that stressful signals in a hostile environment (e.g. acidic and/or dry conditions) can be utilized to induce/enhance virulence gene expression by pathogenic microorganisms. Foodborne pathogens having been exposed to such conditions may become more virulent. We propose to study: 1) Survival of EHEC strains (mainly non-0157:H7) as affected by pH and water activity; and 2) Virulence of EHEC strains as affected by pH and water activity.

9700775 Alternative Landscape Management: Hypothesis, Options, and Returns
Chen, J.; Desanker, P. **Grant 97-35101-4315**

Michigan Technological University **New Investigator Award**
School of Forestry and Wood Products **$220,000**
Houghton, MI 49931 **3 Years**

Different harvesting methods result in different structural patterns across the landscape. Size and placement of patches, corridors, and other features of the landscape are determined in part by the harvesting method implemented on an area. Landscape level effects of stand level management activities are becoming increasingly recognized as important. However, little information currently exists on the effects of these resultant large scale patterns on such critical issues as biodiversity. Therefore, managers have limited understanding of how their actions influence biodiversity and economic returns at broader scales. We propose to

test the hypothesis that landscape structure (i.e., the spatial arrangement of patches, corridors, ecotones, and matrix) directly controls the distribution and diversity of plant species, wildlife habitat quality, and economic output. We will collect field data in a carefully delineated landscape in northern Wisconsin and attempt to develop predictive models between these variables and landscape structure, which will vary as a result of different silvicultural alternatives. These predictive relationships will then be employed in a stand projection model (Forest Vegetation Simulator, FVS) and a harvest allocation model (HARVEST). Feedback based on predictions of ecological and economic values will be used to modify current management alternatives and/or develop other creative plans for the landscape. A workshop for managers and scientists will allow evaluation of landscape designs before and after application of the models. Results can be used
directly by land managers in revising current management guidelines to sustain economic returns while maintaining diversity and habitat quality for both public and private landowners.

9701611 Carbon Concentration Mechanism in Plants and Algae
Goyal, A. **Grant 97-35306-4943**

University of Minnesota, Duluth **New Investigator Award**
Department of Biology **$100,000**
Duluth, MN 55812-2496 **2 Years**

By some estimates aquatic photosynthesis contributes more than 70% of the global CO_2 utilization (fixation + deposition of carbon as carbonate for long term storage). Ambient level of CO_2 in water is insufficient for rapid growth of green algae and aquatic plants; therefore mechanisms for concentrating dissolved inorganic carbon (DIC) are present to increase the rate of photosynthesis and to suppress photorespiration, an energetically wasteful process in plants and algae. An unsolved problem in photosynthesis research is how dissolved inorganic carbon is concentrated by aquatic plants and green algae. We have identified two proteins (LCI-45 and LCI-47) that are likely to be involved in active inorganic carbon transport into the chloroplasts, the site of CO_2 fixation. The proposed research is aimed at confirming and characterizing the function of these two proteins. The long term goal of our research program is to understand the structure and function of the components of aquatic DIC-concentrating mechanism(s). An additional goal is to evaluate feasibility of transferring genes encoding components of DIC transport system to C-3 plants of economic importance. A genetically engineered active inorganic carbon transport system may reduce photorespiration that may result in more photosynthetic biomass production and a lowering of the atmospheric CO_2 equilibrium.

9701727 Nondestructive Monitoring of Hybrid Corn Possessing Genetically Modified Starch
Campbell, M.R. **Grant 97-35503-4753**

Truman State University **New Investigator/Strengthening Award**
Division of Science **$61,894**
Kirksville, MO 63501-4221 **2 Years**

Most corn in the United States is used as animal feed, however, in recent years an increasing amount has been refined in order to produce various food and nonfood products. Starch, a major product from corn refining, is a raw ingredient for manufacturing many of these. Some examples include corn sweeteners, biodegradable packing materials, fuel ethanol and modified starches used in processed foods. Corn farmers in the United States directly benefit from these uses because it increases the demand for corn and the profitability of farming. To further expand the use of corn, scientists have developed hybrids with genetically modified starch. In the food industry there are several advantages in using these. For example, they do not require regulatory approval and they have fewer problems associated with consumer acceptance since they are "all natural." As the acreage of genetically modified starch hybrids increases, a major obstacle limiting their availability to industrial processors is keeping it separated from normal corn during grain transportation and storage. Those involved in handling grain would greatly benefit from a method to monitor the purity and avoid contamination. The objective of this research is to provide the grain industry with a rapid, non-destructive method to test the purity of these hybrids. We plan to investigate the use of Near-Infrared Transmittance Spectroscopy (NITS). Using numerous corn varieties we will try to calibrate the instrument so it will "recognize" hybrids with genetically different starch. Many elevators and grain processing facilities currently have NITS instruments in operation for routine testing of protein, starch and oil content. If the NITS instrument can be calibrated for starch quality characteristics from our research, instruments used in industrial settings could simply load our calibration with minimal additional expense or training.

9700735 Quantifying an Ecosystem Perturbation: Forests, Mycorrhizae, and Red-Backed Voles
Mills, L.S. **Grant 97-35101-4355**

University of Montana
Wildlife Biology Program
Missoula, MT 59812

New Investigator/Strengthening Award
$120,000
2 Years

Forest ecosystems have received special attention in the Pacific Northwest since President Clinton convened a special scientific panel to evaluate how management will affect forests and wildlife. One of the most crucial biotic components of Northwest forest ecosystems involves the dynamics of red-backed voles, which are a primary dispersal vector for the fruiting bodies of mycorrhizal fungi (truffles). Mycorrhizae are, in turn, essential for tree regeneration following harvest. Previous work has shown that California red-backed voles are infrequent near edges of forest remnants and absent from the clearcuts surrounding remnants in SW Oregon, but positively associated with truffles and decaying logs within the remnants. At the same time, truffles are lacking from clearcuts, most likely to be found under logs, and infrequent on the edges of forest remnants. The proposed work will fill in two gaps critical to forest sustainability. First, I will evaluate whether the striking demonstrations of negative edge effects and isolation for red-backed voles in 1990/1991 still hold nearly a decade later. Second, I will use large, replicated trapping grids to assess whether the observed negative edge effects translate into decreased birth and survival rates for red-backed voles in forest interiors relative to those on the edge, implying a demographic "sink." Such information will not only provide insight into demographic feedback between forest system perturbation and the persistence of red-backed voles, but it will also help establish protocols for long-term monitoring a species that is pivotal in Northwest forest ecosystems.

9701353 Nucleotide Diversity in *Brassica oleracea* Floral Homeotic Genes
Purugganan, M.D. **Grant 97-35301-4688**

North Carolina State University
Department of Genetics
Raleigh, NC 27695-7614

New Investigator Award
$100,000
2 Years

The domestication of crop plant species is usually associated with changes in plant form and structure. The genetic basis behind these transformations in plant morphology, however, remains poorly understood. It appears likely, though, that many of these structural changes result from alterations in genes that regulate developmental systems. Diversity at these regulatory genes can thus be expected to affect the rate at which selection, both natural and artificial, can operate. We will investigate the molecular population genetics of structural variation in floral homeotic genes that control the development of the altered inflorescence architectures within the cole crop species *Brassica oleracea*. Our approach will be to sample alleles for the *CAULIFLOWER* (*BoCAL*) gene, and sequence these alleles from both wild and cultivated subspecies within *B. oleracea*, including cauliflower and broccoli. The extent and patterning of sequence diversity between alleles will be used to learn more about the origin and history of different subspecies, and to examine the degree to which population genetic forces such as mutation, recombination, selection, genetic drift and gene flow interact at these floral homeotic loci. This study will provide information on how domestication affects the structure of genetic diversity of crop plant populations, and permit us to design more rational and targeted strategies for germplasm conservation. This population genetic approach should also furnish insights into the molecular evolutionary bases of morphological variation that characterizes the diversification of crop plant species.

9701311 The Role of a Family of Nuclear-Encoded Sigma Factors in Plastid Transcription Regulation
Allison, L.A. **Grant 97-35301-4514**

University of Nebraska
Department of Biochemistry
Lincoln, NE 68538-0664

New Investigator Award
$130,000
2 Years

Coordinated expression of photosynthetic components in response to environmental signals such as light has a profound impact on plant efficiency and crop yield. In chloroplasts, the photosynthetic organelles of plants, some genes which encode proteins of the photosynthetic apparatus are expressed in a light-responsive manner. In part, this enhanced gene expression is due to light-regulated RNA synthesis by the chloroplast RNA polymerase. It is still not clear how the RNA polymerase is directed to transcribe specific genes in the light. One model suggests that RNA polymerase selects particular genes by interacting with specific selectivity proteins known as sigma factors. These sigma factors, encoded in the nuclear DNA, may themselves be differentially expressed in response to light or developmental cues. The aim of this proposal is to investigate the role of a family of sigma factors in regulating chloroplast transcription in the model plant, *Arabidopsis thaliana*. Three sigma factor cDNAs have been isolated from this plant and will be used to address the following questions: i) are the encoded proteins targeted to the chloroplast compartment; ii) do they associate with the chloroplast RNA polymerase; iii) are they differentially expressed? In addition, by manipulating (reducing or increasing) the synthesis of each of the sigma factors in *Arabidopsis* we can ask which subset of chloroplast genes requires each of the sigma factor proteins for expression. In this way we will begin to understand how genes

in the nuclear compartment of a plant cell can control environmentally-regulated expression of genes in the chloroplast compartment.

9702974 Moisture Transport in Paper Materials Under Dynamic Conditions
Chatterjee, S.G. **Grant 97-35504-4795**

SUNY College of Environmental Science & Forestry **New Investigator/Strengthening Award**
Faculty of Paper Science and Engineering **$60,000**
Syracuse, NY 13210 **2 Years**

The moisture content of a paper sheet or board is a key parameter which affects its mechanical and electrical properties. There is a severe loss in the strength properties of paper with increasing moisture content which is accentuated under cyclic humidity conditions. We propose detailed experimental and theoretical investigations in (1) moisture sorption equilibria with special attention to the interior of the hysteresis region, (2) transport mechanisms of moisture through paper webs, and (3) the uptake and release of moisture under ramp and cyclic changes of the relative humidity (RH) of the external environment. In order to understand and quantify moisture changes occurring in a paper board under a changing external RH, all of the above three areas are linked to one another and have to be studied systematically.

The outcome of the research will be a coherent body of knowledge about the hysteresis observed in the equilibrium moisture content under equilibrium RH conditions and the mechanisms of moisture transport in paper under dynamic RH conditions. This will enable paper physicists to relate the effects of changing RH to the warp and dimensional stability of paperboard cartons and lead to better design of packaging materials. The research proposed here will be useful in developing consistent pre-conditioning procedures for paper samples in paper testing laboratories and will also be applicable to the drying of wood and paper, thus leading to their better utilization.

9701228 Signal Transduction Pathways Controlling Plant Growth Adaptations to Water Deficit
Conley, T.R. **Grant 97-35100-4227**

Oklahoma City University **New Investigator/Strengthening Award**
Department of Biology **$110,700**
Oklahoma City, OK 73106-1493 **2 Years**

When a corn seedling lacks sufficient water for normal growth, elongation of the shoot decreases or stops altogether. In contrast, the root system of the seedling continues to grow, presumably as a means of finding water and bringing it to the plant. The regulatory mechanism that controls plant growth adjustments to water stress is unknown. In responding to other environmental cues, such as light and temperature stress, plants utilize signaling pathways that are similar to those used by yeast and animals. It is likely that plants use similar processes to control their responses to water stress One important class of molecules that participates in virtually all signaling pathways is that of the protein kinases. The focus of this project is the isolation of a protein kinase that is rapidly activated by water stress in the roots of corn seedlings. This protein kinase is found in the roots before the onset of water stress and is activated in the region of the root where growth occurs. Preliminary work has shown that this molecule may function as a switch at an early step in controlling the growth adjustments of water-stressed corn seedlings. Isolating this protein may be an important step towards understanding how plants control their responses to drought and may facilitate progress towards genetic manipulation of plants with improved drought tolerance.

9706631 Determinants of Sapwood Quantity in Douglas-fir
Gartner, B.L. **Grant 97-35103-5052**
PECASE* Awardee 1996

Oregon State University **1997 Award: $118,465**
Department of Forest Products **$182,438**
Corvallis, OR 97331-7402 **3 Years**

This research investigates the structure and physiology of sapwood as a function of its location within the tree to elucidate the "design criteria" of Douglas-fir (*Pseudotsuga menziesii*) for sapwood quantity. Whether a specimen is sapwood or heartwood has a major effect on how the wood is processed and used. Previous studies suggest that trees maintain either a constant ratio of leaf area to sapwood area, or, if the sapwood has variable permeability within a tree, constant leaf area/sapwood conductance (where conductance is area times its permeability). However, our initial research in 29-year old trees, shows that permeability did indeed vary from location to location, but that neither leaf area/sapwood area nor leaf area/sapwood conductance was the same for adjacent plantations at different tree densities, nor within one tree.

It is possible that trees adjust their sapwood area for a) water transport in the summer when some of the conduits are embolized, and/or b) a constant storage capacity per leaf area. This project is designed to distinguish between the two hypotheses regarding sapwood determinants, either that sapwood quantity is determined by water transport, or by storage. We will measure volumetric storage and respiration rates, and conductance and loss of conductance due to cavitation, for trees as a function of

season and the leaf area they supply. The trees will come from age and/or aridity gradients. This research will help us predict sapwood quantity of trees from different silvicultural regimes, which will be of use to processors and users of forest products, tree physiologists, and ecosystem modelers.

*Presidential Early Career Awards for Scientists and Engineers

9701367 Genetic Components Required for Paramutation at the Maize *pl* Locus
Hollick, J.B. **Grant 97-35301-4430**

University of Oregon **New Investigator Award**
Institute of Molecular Biology **$ 140,000**
Eugene, OR 97403-1229 **2 Years**

The genesis, maintenance, and manipulation of genetic variation are of primary agronomic importance. Yet the very nature of genetic variation is poorly understood. This work addresses an example where variation is exhibited by a single gene. The *pl* (*purple plant*) gene in corn controls the production of purple pigment. One allele (a particular form) of the *pl* gene can exhibit a range of activities conferring weak to intense coloration. Particular levels of activity are heritably changed through interactions with the other *pl* allele; this influence of one allele on another is called paramutation. Thus, using certain combinations of *pl* alleles, plant color can be either enhanced or reduced. This is reminiscent of the processes of inbreeding depression and heterosis (hybrid vigor); it is expected that these studies on an experimentally amenable pigment gene will lend insights into the mechanistic basis of both processes. The long term goal of this work is to elucidate the molecular basis of these allelic interactions that occur during paramutation; what DNA sequences are required and what cellular proteins mediate the process. As a first step, mutations affecting *pl* paramutation have been identified. Some of these mutations reside within the *pl* gene and others reside in different genes; together these mutations address the above goals. The primary aim of this project is to further characterize these mutations and their effects on paramutation. Results of this study will identify molecular models which can subsequently be tested. A thorough understanding of this process should eventually lead to novel approaches for both traditional and marker-assisted breeding strategies.

9701358 Biochemical and Biophysical Characterization of *Arabidopsis* MADS Domain Proteins
Krizek, B.A. **Grant 97-35304-4690**

University of South Carolina, Columbia **New Investigator Award/Strengthening Award**
Department of Biological Sciences **$90,000**
Columbia, SC 29208-001 **2 Years**

Molecular genetic studies in the model plant *Arabidopsis thaliana* have identified a family of genes that play important roles in flower development. Two members of this MADS box family, *APETALA3* (*AP3*) and *PISTILLATA* (*PI*), are required for the development of petals and stamen in a flower. AP3 and PI form a heterodimer that binds to DNA and is thought to act as a transcription factor, regulating the expression of a set of genes required for organ development. Although AP3 and PI form homodimers, *in vitro* data indicates that the homodimers do not bind DNA. To understand the basis for this DNA-binding specificity, biochemical and biophysical characterization of the proteins is necessary. We will develop an expression system for AP3 and PI so that these methods will be possible in the future. Molecular modeling of the AP3/PI heterodimer, based upon the known structure of another MADS domain protein, will be performed in order to identify amino acids that may be responsible for the ability of the heterodimer but not the homodimers to bind DNA. The role of these amino acids will be investigated by making mutations at these positions and assaying the resulting sequence variants in *in vitro* DNA-binding studies and in vivo for their ability to rescue the respective (*ap3* or *pi*) mutant. Characterization of the interactions between MADS domain proteins that result in DNA binding dimers is a first step towards understanding the regulatory roles of MADS domain proteins in plant development.

9704035 Postnatal Involution of Brown Fat in *Bos taurus* and *Bos indicus* Calves
Smith, S.B.; Carstens, G.E. **Grant 97-35206-5134**

Texas A&M University **New Investigator Award**
Department of Animal Science **$100,000**
College Station, TX 77843-2471 **2 Years**

Suboptimal growth and development are limiting factors in animal productivity, and neonatal calf mortality losses represent a major biological restraint to beef cattle production. In Texas alone, current estimates indicate that approximately 432,000 calves die annually during the neonatal period, which results in revenue losses of more than $200 million. This is particularly significant for beef producers in Texas, since more than half of the 5.4 million beef cows in Texas are Brahman or Brahman crossbred cattle. *Bos indicus* cattle are more susceptible to neonatal losses than *Bos taurus* cattle. Brown adipose tissue (BAT) thermogenesis is

an important component for proper thermoregulation during the early neonatal period. Although our knowledge of the mechanisms controlling BAT thermogenic function in laboratory animals has advanced greatly in recent years, much less is known about these regulatory mechanisms in ruminant neonates. We propose and will test the following hypotheses regarding possible mechanisms that contribute to dysfunctional BAT thermogenesis in Brahman calves. First, thermogenic capacity, *beta*-adrenergic receptor populations, and UP gene expression will decline more rapidly early postnatally in Brahman calves than in Angus calves, especially in response to cold exposure. Second, Brahman BAT will exhibit lesser capacity to synthesize and, especially, oxidize fatty acids in vitro than Angus BAT early postnatally and in response to cold exposure. This also will be reflected in the morphological characteristics of the BAT depots. This research will provide specific information on the regulation of lipid turnover and adipocyte differentiation at the cellular level. This proposal also is a carefully designed investigation of the cellular and molecular aspects of the effects of the environment (*i.e.*, cold vs. warm exposure) on adipose tissue growth and development. Elucidation of these regulatory mechanisms eventually will lead to the development of strategies to enhance BAT function, thereby improving cold tolerance and survivability of newborn calves during inclement weather.

9701932 Genetic Analysis of New Mutants Affecting Light Signaling and Development
Pepper, A.E. **Grant 97-35304-4693**

Texas A & M University **New Investigator Award**
Department of Biology **$ 95,000**
College Station, TX 77843-3258 **2 Years**

Understanding how light influences plant growth and development is essential to future crop improvement strategies. In order to study the molecular pathways by which light directs plant growth, a combined molecular-biological and genetic approach has been initiated to study light regulation of seedling development (de-etiolation) in the small crucifer *Arabidopsis thaliana*. Previous screens for genetic mutants have led to the identification of genes for a red/far-red photoreceptor called phytochrome (*PHYA*, *PHYB*), a blue/ultraviolet photoreceptor called cryptochrome (*CRY1*), and regulatory molecules located in the nucleus such as *de-etiolated* (*DET1*) and *constitutive photomorphogenesis* (*COP1*). Little information about the possible signaling steps in-between, such as the initial steps in phytochrome and cryptochrome signaling, has thus far been obtained through genetics. Genetic screens for second site (extragenic) mutations that suppress the phenotype of a known mutation have proven to be a valuable strategy for the elucidation of complex genetic regulatory pathways in bacteria, yeast, and the fruit fly. To further define the pathway for light regulation of seedling development we have isolated extragenic mutations that suppress the phenotype of *det1*. These have been designated *ted1* through *ted5*. In order to more fully understand the role of *TED1* and *DET1* in the context of the molecular pathways that mediate light regulation of seedling development, we propose to identify, and obtain DNA and protein sequence from the *TED1* gene, and to characterize the biochemical and genetic interactions of *TED1* with *DET1* and other known genes involved in light regulation, including *COP1*, *PHYA*, *PHYB* and *CRY1*.

9702832 Contribution of UV-light Resistance to Epiphytic Fitness in *Pseudomonas syringae*
Sundin, G.W. **Grant 97-35316-5140**

Texas A&M University **New Investigator Award**
Department of Plant Pathology and Microbiology **$100,000**
College Station, TX 77843-2132 **2 Years**

Strains of the plant-pathogenic bacterium *Pseudomonas syringae* cause economically important losses to crop productivity by inciting disease and by catalyzing frost injury. An important prerequisite to infection of leaves and other aerial plant surfaces by *P. syringae* is the development of large epiphytic populations on symptomless leaf surfaces. While the role of epiphytic populations in the disease epidemiology of *P. syringae* is firmly established, the specific phenotypic adaptations of *P. syringae* required for survival and growth in the leaf surface environment (phyllosphere) have received less attention. Recently, we identified a plasmid-encoded operon, rulAB, which significantly increases the tolerance of *P. syringae* to the lethal consequences effected by exposure to ultraviolet light (UV). The rulAB operon encodes a repair mechanism which recognizes and repairs DNA damage induced by UV irradiation. The ability to combat exposure to UV by *P. syringae* is important since the phyllosphere environment is subjected to abnormally high doses of incipient UV radiation compared to other microbial habitats. Thus, we anticipate that knowledge of how expression of rulAB modulates leaf surface growth and survival of *P. syringae* will contribute to our overall understanding of the interplay between epiphytic growth and pathogenesis in this organism. Such knowledge is critical to the development and implementation of successful management strategies aimed at controlling diseases incited by this bacterium.

9700578 Environmental Influences on Children's Diets
Cullen, K.W. **Grant 97-35200-4233**

University of Texas M.D. Anderson Cancer Center
Department of Behavioral Science
Houston, TX 77030-4095

New Investigator Award
$80,000
2 Years

Inadequate intake of fruit and vegetables and high intake of dietary fat are associated with increased risks for cancer. Children eat fewer fruit and vegetables and more fat than recommended. Research has revealed that personal factors are only low predictors of fruit and vegetable consumption, suggesting that environmental factors may be important in understanding children's food consumption. Little is known about how environmental factors influence children's food consumption. This pilot study will identify how three environmental factors (parent motivation, knowledge, and skills to promote healthy diets in children, food availability/accessibility, and social factors) influence 9-12 year old children's fruit, vegetable, and fat consumption. In the first year, focus groups will be conducted with African-American, Euro-American, and Mexican-American 4th-6th grade children and their parents to investigate dietary practices and develop and test survey questions on environmental influences on food intake. In year 2, another group of African-American, Euro-American, and Mexican-American 4th-6th grade students will complete 7-day food records and the social influences questionnaire. Availability/accessibility of the target foods in the school cafeteria and in fast food and other restaurants commonly identified in the children's food records will be assessed by observation. Parent motivation, knowledge, and skills to promote children's healthy diets and home availability/accessibility of the target foods will be obtained by phone data collection from parents. The environmental factors will be related to consumption and compared across ethnic groups. If environmental factors substantially influence children's diet, interventions will need to target them to be successful.

9701771 Interaction and Organization of Zeins in Maize Protein Bodies
Coleman, C.E. **Grant 97-35301-4222**

Brigham Young University
Department of Botany
Provo, UT 84602

New Investigator Award/Strengthening Award
$100,000
2 Years

Zeins are proteins produced in maize grain that are used by the seed to store nitrogen and amino acids for the germinating seedling. Approximately 50-60% of seed proteins are zeins. These proteins do not contain lysine or tryptophan, which are essential amino acids in the diet of humans, non-ruminant livestock and poultry. The reduced amount of these amino acids makes the grain nutritionally deficient. Zeins are packaged as spherical bodies within the cells of the seed's nutritive tissue. Disruptions in the way zeins are packaged lead to profound changes in the physical properties of the seed, all of which are detrimental to the commercial viability of the grain. It is the purpose of this project to study the interactions between zein proteins that lead to the formation of the spherical protein bodies. The project is also designed to learn whether the zein proteins can be altered, specifically by adding lysine and tryptophan amino acids, without significant interruption of their packing arrangement. These goals will be accomplished by transferring normal and altered forms of the zein genes into tobacco plants. Interactions between the zein proteins in the seeds of these tobacco plants can then be studied without interference from native proteins. The results from these experiments will provide a basis for future work of genetically introducing modified zein proteins into maize seeds in order to manipulate the balance of amino acids.

9702977 Diffusion of Wood Product Innovations in Residential Construction
Eastin, I.L. **Grant 97-35103-4896**

University of Washington
College of Forest Resources
Seattle, WA 98195-2100

New Investigator Award
$78,000
1 Year

Rising softwood lumber prices, price instability, and perceived declines in softwood lumber quality have reduced the competitiveness of softwood lumber in the residential construction industry. This trend provides an opportunity for softwood lumber substitutes such as engineered wood products to increase their competitive position in the marketplace. Engineered wood products typically utilize lower quality raw material inputs (e.g., small diameter trees and lesser used timber species) to produce a high quality, high performance product. The key to developing markets for these innovative new products is to understand the factors that influence the adoption and diffusion of new construction materials within the residential construction industry. Residential contractors and builders will be surveyed to assess their perceptions of how various factors influence their decision to evaluate and incorporate engineered wood products into their construction practice. The information obtained from the survey will help: (1) determine the extent to which engineered wood products are currently utilized within the residential construction industry, (2) identify those factors that influence the adoption of engineered wood products, (3) identify those product attributes that influence the adoption of engineered wood products, and (4) develop models of the adoption and diffusion process. The

results of this project will facilitate our understanding of how new products are evaluated and adopted by contractors and builders in the residential construction industry and provide a basis for maintaining the competitive position of wood-based materials *vis-à-vis* non-wood substitutes (e.g., steel studs and concrete).